



HENK0060.ST25.txt
SEQUENCE LISTING

<110> Kottwitz, Beatrix
Breves, Roland
Maurer, Karl-Heinz

<120> DETERGENT AND CLEANING AGENT WITH HYBRID ALPHA-AMYLASES

<130> HENK-0060 / H4714

<140> US 10/774,018

<141> 2004-02-06

<150> PCT/EP02/08391

<151> 2002-07-27

<150> EP 101 38 753.9

<151> 2001-08-07

<160> 20

<170> PatentIn version 3.3

<210> 1

<211> 1452

<212> DNA

<213> Bacillus licheniformis

<220>

<221> CDS

<222> (1)..(1449)

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Asn	Asp	Gly	Gln	His	Trp	Lys	Arg	Leu	Gln	Asn	Asp	Ser	Ala	Tyr	Leu	
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gct	gaa	cac	ggt	att	act	gcc	gtc	tgg	att	ccc	ccg	gca	tat	aag	gga	144
Ala	Glu	His	Gly	Ile	Thr	Ala	Val	Trp	Ile	Pro	Pro	Ala	Tyr	Lys	Gly	
		35					40					45				

acg	agc	caa	gcg	gat	gtg	ggc	tac	ggt	gct	tac	gac	ctt	tat	gat	tta	192
Thr	Ser	Gln	Ala	Asp	Val	Gly	Tyr	Gly	Ala	Tyr	Asp	Leu	Tyr	Asp	Leu	
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ggg	gag	ttt	cat	caa	aaa	ggg	acg	gtt	cgg	aca	aag	tac	ggc	aca	aaa	240
Gly	Glu	Phe	His	Gln	Lys	Gly	Thr	Val	Arg	Thr	Lys	Tyr	Gly	Thr	Lys	
65					70					75					80	

gga	gag	ctg	caa	tct	gcg	atc	aaa	agt	ctt	cat	tcc	cgc	gac	att	aac	288
Gly	Glu	Leu	Gln	Ser	Ala	Ile	Lys	Ser	Leu	His	Ser	Arg	Asp	Ile	Asn	
				85					90					95		

gtt	tac	ggg	gat	gtg	gtc	atc	aac	cac	aaa	ggc	ggc	gct	gat	gcg	acc	336
Val	Tyr	Gly	Asp	Val	Val	Ile	Asn	His	Lys	Gly	Gly	Ala	Asp	Ala	Thr	
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gaa	gat	gta	acc	gcg	gtt	gaa	gtc	gat	ccc	gct	gac	cgc	aac	cgc	gta	384
Glu	Asp	Val	Thr	Ala	Val	Glu	Val	Asp	Pro	Ala	Asp	Arg	Asn	Arg	Val	
		115					120					125				

att	tca	gga	gaa	cac	cga	att	aaa	gcc	tgg	aca	cat	ttt	cat	ttt	ccg	432
Ile	Ser	Gly	Glu	His	Arg	Ile	Lys	Ala	Trp	Thr	His	Phe	His	Phe	Pro	

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gac gga acc gat tgg gac gag tcc cga aag ctg aac cgc atc tat aag Asp Gly Thr Asp Trp Asp Glu Ser Arg Lys Leu Asn Arg Ile Tyr Lys 165 170 175	528		
ttt caa gga aag gct tgg gat tgg gaa gtt tcc aat gaa aac ggc aac Phe Gln Gly Lys Ala Trp Asp Trp Glu Val Ser Asn Glu Asn Gly Asn 180 185 190	576		
tat gat tat ttg atg tat gcc gac atc gat tat gac cat cct gat gtc Tyr Asp Tyr Leu Met Tyr Ala Asp Ile Asp Tyr Asp His Pro Asp Val 195 200 205	624		
gca gca gaa att aag aga tgg ggc act tgg tat gcc aat gaa ctg caa Ala Ala Glu Ile Lys Arg Trp Gly Thr Trp Tyr Ala Asn Glu Leu Gln 210 215 220	672		
ttg gac ggt ttc cgt ctt gat gct gtc aaa cac att aaa ttt tct ttt Leu Asp Gly Phe Arg Leu Asp Ala Val Lys His Ile Lys Phe Ser Phe 225 230 235 240	720		
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tat ttg aac aaa aca aat ttt aat cat tca gtg ttt gac gtg ccg ctt Tyr Leu Asn Lys Thr Asn Phe Asn His Ser Val Phe Asp Val Pro Leu 275 280 285	864		
cat tat cag ttc cat gct gca tcg aca cag gga ggc ggc tat gat atg His Tyr Gln Phe His Ala Ala Ser Thr Gln Gly Gly Gly Tyr Asp Met 290 295 300	912		
agg aaa ttg ctg aac agt acg gtc gtt tcc aag cat ccg ttg aaa gcg Arg Lys Leu Leu Asn Ser Thr Val Val Ser Lys His Pro Leu Lys Ala 305 310 315 320	960		
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tcg act gtc caa aca tgg ttt aag ccg ctt gct tac gct ttt att ctc Ser Thr Val Gln Thr Trp Phe Lys Pro Leu Ala Tyr Ala Phe Ile Leu 340 345 350	1056		
aca agg gaa tct gga tac cct cag gtt ttc tac ggg gat atg tac ggg Thr Arg Glu Ser Gly Tyr Pro Gln Val Phe Tyr Gly Asp Met Tyr Gly 355 360 365	1104		
acg aaa gga gac tcc cag cgc gaa att cct gcc ttg aaa cac aaa att Thr Lys Gly Asp Ser Gln Arg Glu Ile Pro Ala Leu Lys His Lys Ile 370 375 380	1152		
gaa ccg atc tta aaa gcg aga aaa cag tat gcg tac gga gca cag cat Glu Pro Ile Leu Lys Ala Arg Lys Gln Tyr Ala Tyr Gly Ala Gln His 385 390 400	1200		
gat tat ttc gac cac cat gac att gtc ggc tgg aca agg gaa ggc gac Asp Tyr Phe Asp His His Asp Ile Val Gly Trp Thr Arg Glu Gly Asp 1248			

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Ser Ser Val Ala Asn Ser Gly Leu Ala Ala Leu Ile Thr Asp Gly Pro	420	425 430	
ggt ggg gca aag cga atg tat gtc ggc cgg caa aac gcc ggt gag aca			1344
Gly Gly Ala Lys Arg Met Tyr Val Gly Arg Gln Asn Ala Gly Glu Thr	435	440 445	
tgg cat gac att acc gga aac cgt tgc gag ccg gtt gtc atc aat tcg			1392
Trp His Asp Ile Thr Gly Asn Arg Ser Glu Pro Val Val Ile Asn Ser	450	455 460	
gaa ggc tgg gga gag ttt cac gta aac ggc ggg tcg gtt tca att tat			1440
Glu Gly Trp Gly Glu Phe His Val Asn Gly Gly Ser Val Ser Ile Tyr	465	470 475 480	
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Val Gln Arg			

<210> 2
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 <213> Bacillus licheniformis

<400> 2

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Ala Glu His Gly Ile Thr Ala Val Trp Ile Pro Pro Ala Tyr Lys Gly	35	40	45	
Thr Ser Gln Ala Asp Val Gly Tyr Gly Ala Tyr Asp Leu Tyr Asp Leu	50	55	60	
Gly Glu Phe His Gln Lys Gly Thr Val Arg Thr Lys Tyr Gly Thr Lys	65	70	75	80
Gly Glu Leu Gln Ser Ala Ile Lys Ser Leu His Ser Arg Asp Ile Asn	85	90	95	
Val Tyr Gly Asp Val Val Ile Asn His Lys Gly Gly Ala Asp Ala Thr	100	105	110	
Glu Asp Val Thr Ala Val Glu Val Asp Pro Ala Asp Arg Asn Arg Val	115	120	125	
Ile Ser Gly Glu His Arg Ile Lys Ala Trp Thr His Phe His Phe Pro	130	135	140	
Gly Arg Gly Ser Thr Tyr Ser Asp Phe Lys Trp His Trp Tyr His Phe	145	150	155	160

Asp Gly Thr Asp Trp₁₆₅ Asp Glu Ser Arg Lys₁₇₀ Leu Asn Arg Ile Tyr₁₇₅ Lys
 Phe Gln Gly Lys₁₈₀ Ala Trp Asp Trp Glu₁₈₅ Val Ser Asn Glu₁₉₀ Asn Gly Asn
 Tyr Asp Tyr₁₉₅ Leu Met Tyr Ala Asp₂₀₀ Ile Asp Tyr Asp His₂₀₅ Pro Asp Val
 Ala Ala₂₁₀ Glu Ile Lys Arg Trp₂₁₅ Gly Thr Trp Tyr Ala₂₂₀ Asn Glu Leu Gln
 Leu₂₂₅ Asp Gly Phe Arg Leu₂₃₀ Asp Ala Val Lys His₂₃₅ Ile Lys Phe Ser Phe₂₄₀
 Leu Arg Asp Trp Val₂₄₅ Asn His Val Arg Glu₂₅₀ Lys Thr Gly Lys Glu₂₅₅ Met
 Phe Thr Val Ala₂₆₀ Glu Tyr Trp Gln Asn₂₆₅ Asp Leu Gly Ala Leu₂₇₀ Glu Asn
 Tyr Leu Asn₂₇₅ Lys Thr Asn Phe Asn₂₈₀ His Ser Val Phe Asp₂₈₅ Val Pro Leu
 His Tyr₂₉₀ Gln Phe His Ala Ala₂₉₅ Ser Thr Gln Gly Gly₃₀₀ Gly Tyr Asp Met
 Arg₃₀₅ Lys Leu Leu Asn Ser₃₁₀ Thr Val Val Ser Lys₃₁₅ His Pro Leu Lys Ala₃₂₀
 Val Thr Phe Val Asp₃₂₅ Asn His Asp Thr Gln₃₃₀ Pro Gly Gln Ser Leu₃₃₅ Glu
 Ser Thr Val Gln₃₄₀ Thr Trp Phe Lys Pro₃₄₅ Leu Ala Tyr Ala Phe₃₅₀ Ile Leu
 Thr Arg Glu₃₅₅ Ser Gly Tyr Pro Gln₃₆₀ Val Phe Tyr Gly Asp₃₆₅ Met Tyr Gly
 Thr Lys₃₇₀ Gly Asp Ser Gln Arg₃₇₅ Glu Ile Pro Ala Leu₃₈₀ Lys His Lys Ile
 Glu₃₈₅ Pro Ile Leu Lys Ala₃₉₀ Arg Lys Gln Tyr Ala₃₉₅ Tyr Gly Ala Gln His₄₀₀
 Asp Tyr Phe Asp His₄₀₅ His Asp Ile Val Gly₄₁₀ Trp Thr Arg Glu Gly₄₁₅ Asp
 Ser Ser Val Ala₄₂₀ Asn Ser Gly Leu Ala₄₂₅ Ala Leu Ile Thr Asp₄₃₀ Gly Pro

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Val Gln Arg

<210> 3
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 <212> DNA
 <213> Bacillus amyloliquefaciens

<220>
 <221> CDS
 <222> (1)..(1449)

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 atc gga atc act gcc gtc tgg att cct ccc gca tac aaa gga ttg agc 144
 Ile Gly Ile Thr Ala Val Trp Ile Pro Pro Ala Tyr Lys Gly Leu Ser
 35 40 45
 caa tcc gat aac gga tac gga cct tat gat ttg tat gat tta gga gaa 192
 Gln Ser Asp Asn Gly Tyr Gly Pro Tyr Asp Leu Tyr Asp Leu Gly Glu
 50 55 60
 ttc cag caa aaa ggg acg gtc aga acg aaa tac ggc aca aaa tca gag 240
 Phe Gln Gln Lys Gly Thr Val Arg Thr Lys Tyr Gly Thr Lys Ser Glu
 65 70 75 80
 ctt caa gat gcg atc ggc tca ctg cat tcc cgg aac gtc caa gta tac 288
 Leu Gln Asp Ala Ile Gly Ser Leu His Ser Arg Asn Val Gln Val Tyr
 85 90 95
 gga gat gtg gtt ttg aat cat aag gct ggt gct gat gca aca gaa gat 336
 Gly Asp Val Val Leu Asn His Lys Ala Gly Ala Asp Ala Thr Glu Asp
 100 105 110
 gta act gcc gtc gaa gtc aat ccg gcc aat aga aat cag gaa act tcg 384
 Val Thr Ala Val Glu Val Asn Pro Ala Asn Arg Asn Gln Glu Thr Ser
 115 120 125
 gag gaa tat caa atc aaa gcg tgg acg gat ttt cgt ttt ccg ggc cgt 432
 Glu Glu Tyr Gln Ile Lys Ala Trp Thr Asp Phe Arg Phe Pro Gly Arg
 130 135 140
 gga aac acg tac agt gat ttt aaa tgg cat tgg tat cat ttc gac gga 480
 Gly Asn Thr Tyr Ser Asp Phe Lys Trp His Trp Tyr His Phe Asp Gly
 145 150 155 160

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gcg gac tgg gat gaa tcc cgg aag atc agc cgc atc ttt aag ttt cgt Ala Asp Trp Asp Glu Ser Arg Lys Ile Ser Arg Ile Phe Lys Phe Arg 165 170 175	528
ggg gaa gga aaa gcg tgg gat tgg gaa gta tca agt gaa aac ggc aac Gly Glu Gly Lys Ala Trp Asp Trp Glu Val Ser Ser Glu Asn Gly Asn 180 185 190	576
tat gac tat tta atg tat gct gat gtt gac tac gac cac cct gat gtc Tyr Asp Tyr Leu Met Tyr Ala Asp Val Asp Tyr Asp His Pro Asp Val 195 200 205	624
gtg gca gag aca aaa aaa tgg ggt atc tgg tat gcg aat gaa ctg tca Val Ala Glu Thr Lys Lys Trp Gly Ile Trp Tyr Ala Asn Glu Leu Ser 210 215 220	672
tta gac ggc ttc cgt att gat gcc gcc aaa cat att aaa ttt tca ttt Leu Asp Gly Phe Arg Ile Asp Ala Ala Lys His Ile Lys Phe Ser Phe 225 230 235 240	720
ctg cgt gat tgg gtt cag gcg gtc aga cag gcg acg gga aaa gaa atg Leu Arg Asp Trp Val Gln Ala Val Arg Gln Ala Thr Gly Lys Glu Met 245 250 255	768
ttt acg gtt gcg gag tat tgg cag aat aat gcc ggg aaa ctc gaa aac Phe Thr Val Ala Glu Tyr Trp Gln Asn Asn Ala Gly Lys Leu Glu Asn 260 265 270	816
tac ttg aat aaa aca agc ttt aat caa tcc gtg ttt gat gtt ccg ctt Tyr Leu Asn Lys Thr Ser Phe Asn Gln Ser Val Phe Asp Val Pro Leu 275 280 285	864
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agg cgt ttg ctg gac ggt acc gtt gtg tcc agg cat ccg gaa aag gcg Arg Arg Leu Leu Asp Gly Thr Val Val Ser Arg His Pro Glu Lys Ala 305 310 315 320	960
gtt aca ttt gtt gaa aat cat gac aca cag ccg gga cag tca ttg gaa Val Thr Phe Val Glu Asn His Asp Thr Gln Pro Gly Gln Ser Leu Glu 325 330 335	1008
tcg aca gtc caa act tgg ttt aaa ccg ctt gca tac gcc ttt att ttg Ser Thr Val Gln Thr Trp Phe Lys Pro Leu Ala Tyr Ala Phe Ile Leu 340 345 350	1056
aca aga gaa tcc ggt tat cct cag gtg ttc tat ggg gat atg tac ggg Thr Arg Glu Ser Gly Tyr Pro Gln Val Phe Tyr Gly Asp Met Tyr Gly 355 360 365	1104
aca aaa ggg aca tcg cca aag gaa att ccc tca ctg aaa gat aat ata Thr Lys Gly Thr Ser Pro Lys Glu Ile Pro Ser Leu Lys Asp Asn Ile 370 375 380	1152
gag ccg att tta aaa gcg cgt aag gag tac gca tac ggg ccc cag cac Glu Pro Ile Leu Lys Ala Arg Lys Glu Tyr Ala Tyr Gly Pro Gln His 385 390 400	1200
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tgg tat gac ata acg ggc aac cgt tca gat act gta aaa atc gga tct	1392
Trp Tyr Asp Ile Thr Gly Asn Arg Ser Asp Thr Val Lys Ile Gly Ser	
450	455 460
gac ggc tgg gga gag ttt cat gta aac gat ggg tcc gtc tcc att tat	1440
Asp Gly Trp Gly Glu Phe His Val Asn Asp Gly Ser Val Ser Ile Tyr	
465	470 475 480
gtt cag aaa taa	1452
Val Gln Lys	

<210> 4
 <211> 483
 <212> PRT
 <213> Bacillus amyloliquefaciens

<400> 4

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Gln Ser Asp Asn Gly Tyr Gly Pro Tyr Asp Leu Tyr Asp Leu Gly Glu	
50 55 60	
Phe Gln Gln Lys Gly Thr Val Arg Thr Lys Tyr Gly Thr Lys Ser Glu	
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Leu Gln Asp Ala Ile Gly Ser Leu His Ser Arg Asn Val Gln Val Tyr	
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Gly Asp Val Val Leu Asn His Lys Ala Gly Ala Asp Ala Thr Glu Asp	
100 105 110	
Val Thr Ala Val Glu Val Asn Pro Ala Asn Arg Asn Gln Glu Thr Ser	
115 120 125	
Glu Glu Tyr Gln Ile Lys Ala Trp Thr Asp Phe Arg Phe Pro Gly Arg	
130 135 140	
Gly Asn Thr Tyr Ser Asp Phe Lys Trp His Trp Tyr His Phe Asp Gly	
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Ala Asp Trp Asp Glu Ser Arg Lys Ile Ser Arg Ile Phe Lys Phe Arg	
165 170 175	

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 Val Ala Glu Thr Lys Lys Trp Gly Ile Trp Tyr Ala Asn Glu Leu Ser
 210 215 220
 Leu Asp Gly Phe Arg Ile Asp Ala Ala Lys His Ile Lys Phe Ser Phe
 225 230 235 240
 Leu Arg Asp Trp Val Gln Ala Val Arg Gln Ala Thr Gly Lys Glu Met
 245 250 255
 Phe Thr Val Ala Glu Tyr Trp Gln Asn Asn Ala Gly Lys Leu Glu Asn
 260 265 270
 Tyr Leu Asn Lys Thr Ser Phe Asn Gln Ser Val Phe Asp Val Pro Leu
 275 280 285
 His Phe Asn Leu Gln Ala Ala Ser Ser Gln Gly Gly Gly Tyr Asp Met
 290 295 300
 Arg Arg Leu Leu Asp Gly Thr Val Val Ser Arg His Pro Glu Lys Ala
 305 310 315 320
 Val Thr Phe Val Glu Asn His Asp Thr Gln Pro Gly Gln Ser Leu Glu
 325 330 335
 Ser Thr Val Gln Thr Trp Phe Lys Pro Leu Ala Tyr Ala Phe Ile Leu
 340 345 350
 Thr Arg Glu Ser Gly Tyr Pro Gln Val Phe Tyr Gly Asp Met Tyr Gly
 355 360 365
 Thr Lys Gly Thr Ser Pro Lys Glu Ile Pro Ser Leu Lys Asp Asn Ile
 370 375 380
 Glu Pro Ile Leu Lys Ala Arg Lys Glu Tyr Ala Tyr Gly Pro Gln His
 385 390 395 400
 Asp Tyr Ile Asp His Pro Asp Val Ile Gly Trp Thr Arg Glu Gly Asp
 405 410 415
 Ser Ser Ala Ala Lys Ser Gly Leu Ala Ala Leu Ile Thr Asp Gly Pro
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 Gly Gly Ser Lys Arg Met Tyr Ala Gly Leu Lys Asn Ala Gly Glu Thr
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Trp Tyr Asp Ile Thr Gly Asn Arg Ser Asp Thr Val Lys Ile Gly Ser
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Val Gln Lys

<210> 5
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<213> Artificial

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Gly Gln His Trp Lys Arg Leu Gln Asn Asp Ala Glu His Leu Ser Asp
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atc ggt att act gcc gtc tgg att ccc ccg gca tat aag gga acg agc 144
Ile Gly Ile Thr Ala Val Trp Ile Pro Pro Ala Tyr Lys Gly Thr Ser
35 40 45
caa gcg gat gtg ggc tac ggt gct tac gac ctt tat gat tta ggg gag 192
Gln Ala Asp Val Gly Tyr Gly Ala Tyr Asp Leu Tyr Asp Leu Gly Glu
50 55 60
ttt cat caa aaa ggg acg gtt cgg aca aag tac ggc aca aaa gga gag 240
Phe His Gln Lys Gly Thr Val Arg Thr Lys Tyr Gly Thr Lys Gly Glu
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ctg caa tct gcg atc aaa agt ctt cat tcc cgc gac att aac gtt tac 288
Leu Gln Ser Ala Ile Lys Ser Leu His Ser Arg Asp Ile Asn Val Tyr
85 90 95
ggg gat gtg gtc atc aac cac aaa ggc ggc gct gat gcg acc gaa gat 336
Gly Asp Val Val Ile Asn His Lys Gly Gly Ala Asp Ala Thr Glu Asp
100 105 110
gta acc gcg gtt gaa gtc gat ccc gct gac cgc aac cgc gta att tca 384
Val Thr Ala Val Glu Val Asp Pro Ala Asp Arg Asn Arg Val Ile Ser
115 120 125
gga gaa cac cga att aaa gcc tgg aca cat ttt cat ttt ccg ggg cgc 432
Gly Glu His Arg Ile Lys Ala Trp Thr His Phe His Phe Pro Gly Arg
130 135 140
ggc agc aca tac agc gat ttt aaa tgg cat tgg tac cat ttt gac gga 480
Gly Ser Thr Tyr Ser Asp Phe Lys Trp His Trp Tyr His Phe Asp Gly
145 150 155 160

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Gly Lys Ala Trp Asp Trp Glu Val Ser Asn Glu Asn Gly Asn Tyr Asp		
180 185 190		
tat ttg atg tat gcc gac atc gat tat gac cat cct gat gtc gca gca	624	
Tyr Leu Met Tyr Ala Asp Ile Asp Tyr Asp His Pro Asp Val Ala Ala		
195 200 205		
gaa att aag aga tgg ggc act tgg tat gcc aat gaa ctg caa ttg gac	672	
Glu Ile Lys Arg Trp Gly Thr Trp Tyr Ala Asn Glu Leu Gln Leu Asp		
210 215 220		
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gta gct gaa tat tgg cag aat gac ttg ggc gcg ctg gaa aac tat ttg	816	
Val Ala Glu Tyr Trp Gln Asn Asp Leu Gly Ala Leu Glu Asn Tyr Leu		
260 265 270		
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Asn Lys Thr Asn Phe Asn His Ser Val Phe Asp Val Pro Leu His Tyr		
275 280 285		
cag ttc cat gct gca tcg aca cag gga ggc ggc tat gat atg agg aaa	912	
Gln Phe His Ala Ala Ser Thr Gln Gly Gly Gly Tyr Asp Met Arg Lys		
290 295 300		
ttg ctg aac agt acg gtc gtt tcc aag cat ccg ttg aaa gcg gtt aca	960	
Leu Leu Asn Ser Thr Val Val Ser Lys His Pro Leu Lys Ala Val Thr		
305 310 315 320		
ttt gtc gat aac cat gat aca cag ccg ggg caa tcg ctt gag tcg act	1008	
Phe Val Asp Asn His Asp Thr Gln Pro Gly Gln Ser Leu Glu Ser Thr		
325 330 335		
gtc caa aca tgg ttt aag ccg ctt gct tac gct ttt att ctc aca agg	1056	
Val Gln Thr Trp Phe Lys Pro Leu Ala Tyr Ala Phe Ile Leu Thr Arg		
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gaa tct gga tac cct cag gtt ttc tac ggg gat atg tac ggg acg aaa	1104	
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355 360 365		
gga gac tcc cag cgc gaa att cct gcc ttg aaa cac aaa att gaa ccg	1152	
Gly Asp Ser Gln Arg Glu Ile Pro Ala Leu Lys His Lys Ile Glu Pro		
370 375 380		
atc tta aaa gcg aga aaa cag tat gcg tac gga gca cag cat gat tat	1200	
Ile Leu Lys Ala Arg Lys Gln Tyr Ala Tyr Gly Ala Gln His Asp Tyr		
385 390 395 400		
ttc gac cac cat gac att gtc ggc tgg aca agg gaa ggc gac agc tcg	1248	
Phe Asp His His Asp Ile Val Gly Trp Thr Arg Glu Gly Asp Ser Ser		
405 410 415		
gtt gca aat tca ggt ttg gcg gca tta ata aca gac gga ccc ggt ggg	1296	
Val Ala Asn Ser Gly Leu Ala Ala Leu Ile Thr Asp Gly Pro Gly Gly		
420 425 430		

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gca aag cga atg tat gtc ggc cgg	caa aac gcc ggt gag aca tgg cat	1344
Ala Lys Arg Met Tyr Val Gly Arg	Gln Asn Ala Gly Glu Thr Trp His	
435	440 445	
gac att acc gga aac cgt tcg gag ccg gtt gtc atc aat tcg gaa ggc	1392	
Asp Ile Thr Gly Asn Arg Ser Glu Pro Val Val Ile Asn Ser Glu Gly		
450	455 460	
tgg gga gag ttt cac gta aac ggc ggg tcg gtt tca att tat gtt caa	1440	
Trp Gly Glu Phe His Val Asn Gly Gly Ser Val Ser Ile Tyr Val Gln		
465	470 475 480	
aga tag	1446	
Arg		

<210> 6
 <211> 481
 <212> PRT
 <213> Artificial

<220>
 <223> Synthetic Construct

<400> 6

Val Asn Gly Thr Leu Met Gln Tyr Phe Glu Trp Tyr Thr Pro Asn Asp	
1 5 10 15	
Gly Gln His Trp Lys Arg Leu Gln Asn Asp Ala Glu His Leu Ser Asp	
20 25 30	
Ile Gly Ile Thr Ala Val Trp Ile Pro Pro Ala Tyr Lys Gly Thr Ser	
35 40 45	
Gln Ala Asp Val Gly Tyr Gly Ala Tyr Asp Leu Tyr Asp Leu Gly Glu	
50 55 60	
Phe His Gln Lys Gly Thr Val Arg Thr Lys Tyr Gly Thr Lys Gly Glu	
65 70 75 80	
Leu Gln Ser Ala Ile Lys Ser Leu His Ser Arg Asp Ile Asn Val Tyr	
85 90 95	
Gly Asp Val Val Ile Asn His Lys Gly Gly Ala Asp Ala Thr Glu Asp	
100 105 110	
Val Thr Ala Val Glu Val Asp Pro Ala Asp Arg Asn Arg Val Ile Ser	
115 120 125	
Gly Glu His Arg Ile Lys Ala Trp Thr His Phe His Phe Pro Gly Arg	
130 135 140	
Gly Ser Thr Tyr Ser Asp Phe Lys Trp His Trp Tyr His Phe Asp Gly	
145 150 155 160	
Thr Asp Trp Asp Glu Ser Arg Lys Leu Asn Arg Ile Tyr Lys Phe Gln	

165

170

175

Gly Lys Ala Trp Asp Trp Glu Val Ser Asn Glu Asn Gly Asn Tyr Asp
 180 185 190

Tyr Leu Met Tyr Ala Asp Ile Asp Tyr Asp His Pro Asp Val Ala Ala
 195 200 205

Glu Ile Lys Arg Trp Gly Thr Trp Tyr Ala Asn Glu Leu Gln Leu Asp
 210 215 220

Gly Phe Arg Leu Asp Ala Val Lys His Ile Lys Phe Ser Phe Leu Arg
 225 230 235 240

Asp Trp Val Asn His Val Arg Glu Lys Thr Gly Lys Glu Met Phe Thr
 245 250 255

Val Ala Glu Tyr Trp Gln Asn Asp Leu Gly Ala Leu Glu Asn Tyr Leu
 260 265 270

Asn Lys Thr Asn Phe Asn His Ser Val Phe Asp Val Pro Leu His Tyr
 275 280 285

Gln Phe His Ala Ala Ser Thr Gln Gly Gly Gly Tyr Asp Met Arg Lys
 290 295 300

Leu Leu Asn Ser Thr Val Val Ser Lys His Pro Leu Lys Ala Val Thr
 305 310 315 320

Phe Val Asp Asn His Asp Thr Gln Pro Gly Gln Ser Leu Glu Ser Thr
 325 330 335

Val Gln Thr Trp Phe Lys Pro Leu Ala Tyr Ala Phe Ile Leu Thr Arg
 340 345 350

Glu Ser Gly Tyr Pro Gln Val Phe Tyr Gly Asp Met Tyr Gly Thr Lys
 355 360 365

Gly Asp Ser Gln Arg Glu Ile Pro Ala Leu Lys His Lys Ile Glu Pro
 370 375 380

Ile Leu Lys Ala Arg Lys Gln Tyr Ala Tyr Gly Ala Gln His Asp Tyr
 385 390 395 400

Phe Asp His His Asp Ile Val Gly Trp Thr Arg Glu Gly Asp Ser Ser
 405 410 415

Val Ala Asn Ser Gly Leu Ala Ala Leu Ile Thr Asp Gly Pro Gly Gly
 420 425 430

Ala Lys Arg Met Tyr Val Gly Arg Gln Asn Ala Gly Glu Thr Trp His
 Page 12

435

440

445

Asp Ile Thr Gly Asn Arg Ser Glu Pro Val Val Ile Asn Ser Glu Gly
 450 455 460

Trp Gly Glu Phe His Val Asn Gly Gly Ser Val Ser Ile Tyr Val Gln
 465 470 475 480

Arg

<210> 7
 <211> 1446
 <212> DNA
 <213> Artificial

<220>
 <223> Fusion of Alpha-Amylase-Gene von B. licheniformis and B.
 amyloliquefaciens (AL76)

<220>
 <221> CDS
 <222> (1)..(1443)

<400> 7
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 Val Asn Gly Thr Leu Met Gln Tyr Phe Glu Trp Tyr Thr Pro Asn Asp
 1 5 10 15
 ggc cag cat tgg aaa cga ttg cag aat gat gcg gaa cat tta tcg gat 96
 Gly Gln His Trp Lys Arg Leu Gln Asn Asp Ala Glu His Leu Ser Asp
 20 25 30
 atc gga atc act gcc gtc tgg att cct ccc gca tac aaa gga ttg agc 144
 Ile Gly Ile Thr Ala Val Trp Ile Pro Pro Ala Tyr Lys Gly Leu Ser
 35 40 45
 caa tcc gat aac gga tac gga cct tat gat ttg tat gat tta gga gaa 192
 Gln Ser Asp Asn Gly Tyr Gly Pro Tyr Asp Leu Tyr Asp Leu Gly Glu
 50 55 60
 ttc cag caa aaa ggg acg gtc aga acg aaa tac ggc aca aaa gga gag 240
 Phe Gln Gln Lys Gly Thr Val Arg Thr Lys Tyr Gly Thr Lys Gly Glu
 65 70 75 80
 ctg caa tct gcg atc aaa agt ctt cat tcc cgc gac att aac gtt tac 288
 Leu Gln Ser Ala Ile Lys Ser Leu His Ser Arg Asp Ile Asn Val Tyr
 85 90 95
 ggg gat gtg gtc atc aac cac aaa ggc ggc gct gat gcg acc gaa gat 336
 Gly Asp Val Val Ile Asn His Lys Gly Gly Ala Asp Ala Thr Glu Asp
 100 105 110
 gta acc gcg gtt gaa gtc gat ccc gct gac cgc aac cgc gta att tca 384
 Val Thr Ala Val Glu Val Asp Pro Ala Asp Arg Asn Arg Val Ile Ser
 115 120 125
 gga gaa cac cga att aaa gcc tgg aca cat ttt cat ttt ccg ggg cgc 432
 Gly Glu His Arg Ile Lys Ala Trp Thr His Phe His Phe Pro Gly Arg
 130 135 140
 ggc agc aca tac agc gat ttt aaa tgg cat tgg tac cat ttt gac gga 480
 Gly Ser Thr Tyr Ser Asp Phe Lys Trp His Trp Tyr His Phe Asp Gly

HENK0060.ST25.txt

145	150	155	160	
acc gat tgg gac gag tcc cga aag ctg aac cgc atc tat aag ttt caa	Thr Asp Trp Asp Glu Ser Arg Lys Leu Asn Arg Ile Tyr Lys Phe Gln			528
	165	170	175	
gga aag gct tgg gat tgg gaa gtt tcc aat gaa aac ggc aac tat gat	Gly Lys Ala Trp Asp Trp Glu Val Ser Asn Glu Asn Gly Asn Tyr Asp			576
	180	185	190	
tat ttg atg tat gcc gac atc gat tat gac cat cct gat gtc gca gca	Tyr Leu Met Tyr Ala Asp Ile Asp Tyr Asp His Pro Asp Val Ala Ala			624
	195	200	205	
gaa att aag aga tgg ggc act tgg tat gcc aat gaa ctg caa ttg gac	Glu Ile Lys Arg Trp Gly Thr Trp Tyr Ala Asn Glu Leu Gln Leu Asp			672
	210	215	220	
ggt ttc cgt ctt gat gct gtc aaa cac att aaa ttt tct ttt ttg cg	Gly Phe Arg Leu Asp Ala Val Lys His Ile Lys Phe Ser Phe Leu Arg			720
	225	230	235	
gat tgg gtt aat cat gtc agg gaa aaa acg ggg aag gaa atg ttt acg	Asp Trp Val Asn His Val Arg Glu Lys Thr Gly Lys Glu Met Phe Thr			768
	245	250	255	
gta gct gaa tat tgg cag aat gac ttg ggc gcg ctg gaa aac tat ttg	Val Ala Glu Tyr Trp Gln Asn Asp Leu Gly Ala Leu Glu Asn Tyr Leu			816
	260	265	270	
aac aaa aca aat ttt aat cat tca gtg ttt gac gtg ccg ctt cat tat	Asn Lys Thr Asn Phe Asn His Ser Val Phe Asp Val Pro Leu His Tyr			864
	275	280	285	
cag ttc cat gct gca tcg aca cag gga ggc ggc tat gat atg agg aaa	Gln Phe His Ala Ala Ser Thr Gln Gly Gly Tyr Asp Met Arg Lys			912
	290	295	300	
ttg ctg aac agt acg gtc gtt tcc aag cat ccg ttg aaa gcg gtt aca	Leu Leu Asn Ser Thr Val Val Ser Lys His Pro Leu Lys Ala Val Thr			960
	305	310	315	
ttt gtc gat aac cat gat aca cag ccg ggg caa tcg ctt gag tcg act	Phe Val Asp Asn His Asp Thr Gln Pro Gly Gln Ser Leu Glu Ser Thr			1008
	325	330	335	
gtc caa aca tgg ttt aag ccg ctt gct tac gct ttt att ctc aca agg	Val Gln Thr Trp Phe Lys Pro Leu Ala Tyr Ala Phe Ile Leu Thr Arg			1056
	340	345	350	
gaa tct gga tac cct cag gtt ttc tac ggg gat atg tac ggg acg aaa	Glu Ser Gly Tyr Pro Gln Val Phe Tyr Gly Asp Met Tyr Gly Thr Lys			1104
	355	360	365	
gga gac tcc cag cgc gaa att cct gcc ttg aaa cac aaa att gaa ccg	Gly Asp Ser Gln Arg Glu Ile Pro Ala Leu Lys His Lys Ile Glu Pro			1152
	370	375	380	
atc tta aaa gcg aga aaa cag tat gcg tac gga gca cag cat gat tat	Ile Leu Lys Ala Arg Lys Gln Tyr Ala Tyr Gly Ala Gln His Asp Tyr			1200
	385	390	395	
ttc gac cac cat gac att gtc ggc tgg aca agg gaa ggc gac agc tcg	Phe Asp His His Asp Ile Val Gly Trp Thr Arg Glu Gly Asp Ser Ser			1248
	405	410	415	
gtt gca aat tca ggt ttg gcg gca tta ata aca gac gga ccc ggt ggg	Val Ala Asn Ser Gly Leu Ala Ala Leu Ile Thr Asp Gly Pro Gly Gly			1296

HENK0060.ST25.txt

420	425	430	
gca aag cga atg tat gtc ggc cgg caa aac gcc ggt gag aca tgg cat			1344
Ala Lys Arg Met Tyr Val Gly Arg Gln Asn Ala Gly Glu Thr Trp His			
435	440	445	
gac att acc gga aac cgt tcg gag ccg gtt gtc atc aat tcg gaa ggc			1392
Asp Ile Thr Gly Asn Arg Ser Glu Pro Val Val Ile Asn Ser Glu Gly			
450	455	460	
tgg gga gag ttt cac gta aac ggc ggg tcg gtt tca att tat gtt caa			1440
Trp Gly Glu Phe His Val Asn Gly Gly Ser Val Ser Ile Tyr Val Gln			
465	470	475	480
aga tag			1446
Arg			

<210> 8
 <211> 481
 <212> PRT
 <213> Artificial

<220>
 <223> Synthetic Construct

<400> 8

Val Asn Gly Thr Leu Met Gln Tyr Phe Glu Trp Tyr Thr Pro Asn Asp	
1 5 10 15	
Gly Gln His Trp Lys Arg Leu Gln Asn Asp Ala Glu His Leu Ser Asp	
20 25 30	
Ile Gly Ile Thr Ala Val Trp Ile Pro Pro Ala Tyr Lys Gly Leu Ser	
35 40 45	
Gln Ser Asp Asn Gly Tyr Gly Pro Tyr Asp Leu Tyr Asp Leu Gly Glu	
50 55 60	
Phe Gln Gln Lys Gly Thr Val Arg Thr Lys Tyr Gly Thr Lys Gly Glu	
65 70 75 80	
Leu Gln Ser Ala Ile Lys Ser Leu His Ser Arg Asp Ile Asn Val Tyr	
85 90 95	
Gly Asp Val Val Ile Asn His Lys Gly Gly Ala Asp Ala Thr Glu Asp	
100 105 110	
Val Thr Ala Val Glu Val Asp Pro Ala Asp Arg Asn Arg Val Ile Ser	
115 120 125	
Gly Glu His Arg Ile Lys Ala Trp Thr His Phe His Phe Pro Gly Arg	
130 135 140	
Gly Ser Thr Tyr Ser Asp Phe Lys Trp His Trp Tyr His Phe Asp Gly	
145 150 155 160	

HENK0060.ST25.txt

Thr Asp Trp Asp Glu Ser Arg Lys Leu Asn Arg Ile Tyr Lys Phe Gln
 165 170 175
 Gly Lys Ala Trp Asp Trp Glu Val Ser Asn Glu Asn Gly Asn Tyr Asp
 180 185 190
 Tyr Leu Met Tyr Ala Asp Ile Asp Tyr Asp His Pro Asp Val Ala Ala
 195 200 205
 Glu Ile Lys Arg Trp Gly Thr Trp Tyr Ala Asn Glu Leu Gln Leu Asp
 210 215 220
 Gly Phe Arg Leu Asp Ala Val Lys His Ile Lys Phe Ser Phe Leu Arg
 225 230 235 240
 Asp Trp Val Asn His Val Arg Glu Lys Thr Gly Lys Glu Met Phe Thr
 245 250 255
 Val Ala Glu Tyr Trp Gln Asn Asp Leu Gly Ala Leu Glu Asn Tyr Leu
 260 265 270
 Asn Lys Thr Asn Phe Asn His Ser Val Phe Asp Val Pro Leu His Tyr
 275 280 285
 Gln Phe His Ala Ala Ser Thr Gln Gly Gly Gly Tyr Asp Met Arg Lys
 290 295 300
 Leu Leu Asn Ser Thr Val Val Ser Lys His Pro Leu Lys Ala Val Thr
 305 310 315 320
 Phe Val Asp Asn His Asp Thr Gln Pro Gly Gln Ser Leu Glu Ser Thr
 325 330 335
 Val Gln Thr Trp Phe Lys Pro Leu Ala Tyr Ala Phe Ile Leu Thr Arg
 340 345 350
 Glu Ser Gly Tyr Pro Gln Val Phe Tyr Gly Asp Met Tyr Gly Thr Lys
 355 360 365
 Gly Asp Ser Gln Arg Glu Ile Pro Ala Leu Lys His Lys Ile Glu Pro
 370 375 380
 Ile Leu Lys Ala Arg Lys Gln Tyr Ala Tyr Gly Ala Gln His Asp Tyr
 385 390 395 400
 Phe Asp His His Asp Ile Val Gly Trp Thr Arg Glu Gly Asp Ser Ser
 405 410 415
 Val Ala Asn Ser Gly Leu Ala Ala Leu Ile Thr Asp Gly Pro Gly Gly
 420 425 430

HENK0060.ST25.txt

Ala Lys Arg Met Tyr Val Gly Arg Gln Asn Ala Gly Glu Thr Trp His
435 440 445

Asp Ile Thr Gly Asn Arg Ser Glu Pro Val Val Ile Asn Ser Glu Gly
450 455 460

Trp Gly Glu Phe His Val Asn Gly Gly Ser Val Ser Ile Tyr Val Gln
465 470 475 480

Arg

<210> 9
<211> 1446
<212> DNA
<213> Artificial

<220>
<223> Fusion of Alpha-Amylase-Gene von B. licheniformis and B. amyloliquefaciens (AL112)

<220>
<221> CDS
<222> (1)..(1443)

<400> 9
gta aat ggc acg ctg atg cag tat ttt gaa tgg tat acg ccg aac gac 48
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1 5 10 15
ggc cag cat tgg aaa cga ttg cag aat gat gcg gaa cat tta tcg gat 96
Gly Gln His Trp Lys Arg Leu Gln Asn Asp Ala Glu His Leu Ser Asp
20 25 30
atc gga atc act gcc gtc tgg att cct ccc gca tac aaa gga ttg agc 144
Ile Gly Ile Thr Ala Val Trp Ile Pro Pro Ala Tyr Lys Gly Leu Ser
35 40 45
caa tcc gat aac gga tac gga cct tat gat ttg tat gat tta gga gaa 192
Gln Ser Asp Asn Gly Tyr Gln Pro Tyr Asp Leu Tyr Asp Leu Gly Glu
50 55 60
ttc cag caa aaa ggg acg gtc aga acg aaa tac ggc aca aaa tca gag 240
Phe Gln Gln Lys Gly Thr Val Arg Thr Lys Tyr Gly Thr Lys Ser Glu
65 70 75 80
ctt caa gat gcg atc ggc tca ctg cat tcc cgg aac gtc caa gta tac 288
Leu Gln Asp Ala Ile Gly Ser Leu His Ser Arg Asn Val Gln Val Tyr
85 90 95
gga gat gtg gtt ttg aat cat aag gct ggt gct gat gca aca gaa gat 336
Gly Asp Val Val Leu Asn His Lys Ala Gly Ala Asp Ala Thr Glu Asp
100 105 110
gta acc gcg gtt gaa gtc gat ccc gct gac cgc aac cgc gta att tca 384
Val Thr Ala Val Glu Val Asp Pro Ala Asp Arg Asn Arg Val Ile Ser
115 120 125
gga gaa cac cga att aaa gcc tgg aca cat ttt cat ttt ccg ggg cgc 432
Gly Glu His Arg Ile Lys Ala Trp Thr His Phe His Phe Pro Gly Arg
130 135 140

HENK0060.ST25.txt

ggc Gly 145	agc Ser	aca Thr	tac Tyr	agc Ser	gat Asp 150	ttt Phe	aaa Lys	tg Trp	cat His	tg Trp 155	tac Tyr	cat His	ttt Phe	gac Asp	gga Gly 160	480
acc Thr	gat Asp	tg Trp	gac Asp	gag Glu 165	tcc Ser	cga Arg	aag Lys	ctg Leu	aac Asn 170	cgc Arg	atc Ile	tat Tyr	aag Lys	ttt Phe 175	caa Gln	528
gga Gly	aag Lys	gct Ala	tg Trp 180	gat Asp	tg Trp	gaa Glu	gtt Val	tcc Ser 185	aat Asn	gaa Glu	aac Asn	ggc Gly	aac Asn 190	tat Tyr	gat Asp	576
tat Tyr	ttg Leu	atg Met 195	tat Tyr	gcc Ala	gac Asp	atc Ile	gat Asp 200	tat Tyr	gac Asp	cat His	cct Pro	gat Asp 205	gtc Val	gca Ala	gca Ala	624
gaa Glu	att Ile 210	aag Lys	aga Arg	tg Trp	ggc Gly	act Thr 215	tg Trp	tat Tyr	gcc Ala	aat Asn	gaa Glu 220	ctg Leu	caa Gln	ttg Leu	gac Asp	672
ggc Gly 225	ttc Phe	cgt Arg	ctt Leu	gat Asp	gct Ala 230	gtc Val	aaa Lys	cac His	att Ile	aaa Lys 235	ttt Phe	tct Ser	ttt Phe	ttg Leu	cgg Arg 240	720
gat Asp	tg Trp	gtt Val	aat Asn	cat His 245	gtc Val	agg Arg	gaa Glu	aaa Lys	acg Thr 250	ggg Gly	aag Lys	gaa Glu	atg Met	ttt Phe 255	acg Thr	768
gta Val	gct Ala	gaa Glu	tat Tyr 260	tg Trp	cag Gln	aat Asn	gac Asp	ttg Leu 265	ggc Gly	gcg Ala	ctg Leu	gaa Glu	aac Asn 270	tat Tyr	ttg Leu	816
aac Asn	aaa Lys	aca Thr 275	aat Asn	ttt Phe	aat Asn	cat His	tca Ser 280	gtg Val	ttt Phe	gac Asp	gtg Val	ccg Pro 285	ctt Leu	cat His	tat Tyr	864
cag Gln	ttc Phe 290	cat His	gct Ala	gca Ala	tcg Ser	aca Thr 295	cag Gln	gga Gly	ggc Gly	ggc Gly	tat Tyr 300	gat Asp	atg Met	agg Arg	aaa Lys	912
ttg Leu 305	ctg Leu	aac Asn	agt Ser	acg Thr	gtc Val 310	gtt Val	tcc Ser	aag Lys	cat His	ccg Pro 315	ttg Leu	aaa Lys	gcg Ala	gtt Val	aca Thr 320	960
ttt Phe	gtc Val	gat Asp	aac Asn	cat His 325	gat Asp	aca Thr	cag Gln	ccg Pro	ggg Gly 330	caa Gln	tcg Ser	ctt Leu	gag Glu	tcg Ser 335	act Thr	1008
gtc Val	caa Gln	aca Thr	tg Trp 340	ttt Phe	aag Lys	ccg Pro	ctt Leu	gct Ala 345	tac Tyr	gct Ala	ttt Phe	att Ile	ctc Leu 350	aca Thr	agg Arg	1056
gaa Glu	tct Ser	gga Gly 355	tac Tyr	cct Pro	cag Gln	gtt Val	ttc Phe 360	tac Tyr	ggg Gly	gat Asp	atg Met	tac Tyr 365	ggg Gly	acg Thr	aaa Lys	1104
gga Gly	gac Asp 370	tcc Ser	cag Gln	cgc Arg	gaa Glu	att Ile 375	cct Pro	gcc Ala	ttg Leu	aaa Lys	cac His 380	aaa Lys	att Ile	gaa Glu	ccg Pro	1152
atc Ile 385	tta Leu	aaa Lys	gcg Ala	aga Arg	aaa Lys 390	cag Gln	tat Tyr	gcg Ala	tac Tyr	gga Gly 395	gca Ala	cag Gln	cat His	gat Asp	tat Tyr 400	1200
ttc Phe	gac Asp	cac His	cat His	gac Asp 405	att Ile	gtc Val	ggc Gly	tg Trp	aca Thr 410	agg Arg	gaa Glu	ggc Gly	gac Asp	agc Ser 415	tcg Ser	1248

HENK0060.ST25.txt

gtt gca aat tca ggt ttg gcg gca tta ata aca gac gga ccc ggt ggg	1296
Val Ala Asn Ser Gly Leu Ala Ala Leu Ile Thr Asp Gly Pro Gly Gly	
420 425 430	
gca aag cga atg tat gtc ggc cgg caa aac gcc ggt gag aca tgg cat	1344
Ala Lys Arg Met Tyr Val Gly Arg Gln Asn Ala Gly Glu Thr Trp His	
435 440 445	
gac att acc gga aac cgt tcg gag ccg gtt gtc atc aat tcg gaa ggc	1392
Asp Ile Thr Gly Asn Arg Ser Glu Pro Val Val Ile Asn Ser Glu Gly	
450 455 460	
tgg gga gag ttt cac gta aac ggc ggg tcg gtt tca att tat gtt caa	1440
Trp Gly Glu Phe His Val Asn Gly Gly Ser Val Ser Ile Tyr Val Gln	
465 470 475 480	
aga tag	1446
Arg	

<210> 10
 <211> 481
 <212> PRT
 <213> Artificial

<220>
 <223> Synthetic Construct

<400> 10

Val Asn Gly Thr Leu Met Gln Tyr Phe Glu Trp Tyr Thr Pro Asn Asp	
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20 25 30	
Ile Gly Ile Thr Ala Val Trp Ile Pro Pro Ala Tyr Lys Gly Leu Ser	
35 40 45	
Gln Ser Asp Asn Gly Tyr Gly Pro Tyr Asp Leu Tyr Asp Leu Gly Glu	
50 55 60	
Phe Gln Gln Lys Gly Thr Val Arg Thr Lys Tyr Gly Thr Lys Ser Glu	
65 70 75 80	
Leu Gln Asp Ala Ile Gly Ser Leu His Ser Arg Asn Val Gln Val Tyr	
85 90 95	
Gly Asp Val Val Leu Asn His Lys Ala Gly Ala Asp Ala Thr Glu Asp	
100 105 110	
Val Thr Ala Val Glu Val Asp Pro Ala Asp Arg Asn Arg Val Ile Ser	
115 120 125	
Gly Glu His Arg Ile Lys Ala Trp Thr His Phe His Phe Pro Gly Arg	
130 135 140	
Gly Ser Thr Tyr Ser Asp Phe Lys Trp His Trp Tyr His Phe Asp Gly	

HENK0060.ST25.txt

145	150	155	160
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Thr Asp Trp Asp Glu Ser Arg Lys Leu Asn Arg Ile Tyr Lys Phe Gln
165 170 175

Gly Lys Ala Trp Asp Trp Glu Val Ser Asn Glu Asn Gly Asn Tyr Asp
180 185 190

Tyr Leu Met Tyr Ala Asp Ile Asp Tyr Asp His Pro Asp Val Ala Ala
195 200 205

Glu Ile Lys Arg Trp Gly Thr Trp Tyr Ala Asn Glu Leu Gln Leu Asp
210 215 220

Gly Phe Arg Leu Asp Ala Val Lys His Ile Lys Phe Ser Phe Leu Arg
225 230 235 240

Asp Trp Val Asn His Val Arg Glu Lys Thr Gly Lys Glu Met Phe Thr
245 250 255

Val Ala Glu Tyr Trp Gln Asn Asp Leu Gly Ala Leu Glu Asn Tyr Leu
260 265 270

Asn Lys Thr Asn Phe Asn His Ser Val Phe Asp Val Pro Leu His Tyr
275 280 285

Gln Phe His Ala Ala Ser Thr Gln Gly Gly Gly Tyr Asp Met Arg Lys
290 295 300

Leu Leu Asn Ser Thr Val Val Ser Lys His Pro Leu Lys Ala Val Thr
305 310 315 320

Phe Val Asp Asn His Asp Thr Gln Pro Gly Gln Ser Leu Glu Ser Thr
325 330 335

Val Gln Thr Trp Phe Lys Pro Leu Ala Tyr Ala Phe Ile Leu Thr Arg
340 345 350

Glu Ser Gly Tyr Pro Gln Val Phe Tyr Gly Asp Met Tyr Gly Thr Lys
355 360 365

Gly Asp Ser Gln Arg Glu Ile Pro Ala Leu Lys His Lys Ile Glu Pro
370 375 380

Ile Leu Lys Ala Arg Lys Gln Tyr Ala Tyr Gly Ala Gln His Asp Tyr
385 390 395 400

Phe Asp His His Asp Ile Val Gly Trp Thr Arg Glu Gly Asp Ser Ser
405 410 415

Val Ala Asn Ser Gly Leu Ala Ala Leu Ile Thr Asp Gly Pro Gly Gly
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420

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425

430

Ala Lys Arg Met Tyr Val Gly Arg Gln Asn Ala Gly Glu Thr Trp His
 435 440 445

Asp Ile Thr Gly Asn Arg Ser Glu Pro Val Val Ile Asn Ser Glu Gly
 450 455 460

Trp Gly Glu Phe His Val Asn Gly Gly Ser Val Ser Ile Tyr Val Gln
 465 470 475 480

Arg

<210> 11
 <211> 1452
 <212> DNA
 <213> Artificial

<220>
 <223> Fusion of Alpha-Amylase-Gene von B. licheniformis and B. amyloliquefaciens (AL256)

<220>
 <221> CDS
 <222> (1)..(1449)

<400> 11
 gta aat ggc acg ctg atg cag tat ttt gaa tgg tat acg ccg aac gac 48
 Val Asn Gly Thr Leu Met Gln Tyr Phe Glu Trp Tyr Thr Pro Asn Asp
 1 5 10 15
 ggc cag cat tgg aaa cga ttg cag aat gat gcg gaa cat tta tcg gat 96
 Gly Gln His Trp Lys Arg Leu Gln Asn Asp Ala Glu His Leu Ser Asp
 20 25 30
 atc gga atc act gcc gtc tgg att cct ccc gca tac aaa gga ttg agc 144
 Ile Gly Ile Thr Ala Val Trp Ile Pro Pro Ala Tyr Lys Gly Leu Ser
 35 40 45
 caa tcc gat aac gga tac gga cct tat gat ttg tat gat tta gga gaa 192
 Gln Ser Asp Asn Gly Tyr Gly Pro Tyr Asp Leu Tyr Asp Leu Gly Glu
 50 55 60
 ttc cag caa aaa ggg acg gtc aga acg aaa tac ggc aca aaa tca gag 240
 Phe Gln Gln Lys Gly Thr Val Arg Thr Lys Tyr Gly Thr Lys Ser Glu
 65 70 75 80
 ctt caa gat gcg atc ggc tca ctg cat tcc cgg aac gtc caa gta tac 288
 Leu Gln Asp Ala Ile Gly Ser Leu His Ser Arg Asn Val Gln Val Tyr
 85 90 95
 gga gat gtg gtt ttg aat cat aag gct ggt gct gat gca aca gaa gat 336
 Gly Asp Val Val Leu Asn His Lys Ala Gly Ala Asp Ala Thr Glu Asp
 100 105 110
 gta act gcc gtc gaa gtc aat ccg gcc aat aga aat cag gaa act tcg 384
 Val Thr Ala Val Glu Val Asn Pro Ala Asn Arg Asn Gln Glu Thr Ser
 115 120 125
 gag gaa tat caa atc aaa gcg tgg acg gat ttt cgt ttt ccg ggc cgt 432
 Glu Glu Tyr Gln Ile Lys Ala Trp Thr Asp Phe Arg Phe Pro Gly Arg
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HENK0060.ST25.txt

130	135	140	
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gcg gac tgg gat gaa tcc cgg aag atc agc cgc atc ttt aag ttt cgt Ala Asp Trp Asp Glu Ser Arg Lys Ile Ser Arg Ile Phe Lys Phe Arg 165 170 175			528
ggg gaa gga aaa gcg tgg gat tgg gaa gta tca agt gaa aac ggc aac Gly Glu Gly Lys Ala Trp Asp Trp Glu Val Ser Ser Glu Asn Gly Asn 180 185 190			576
tat gac tat tta atg tat gct gat gtt gac tac gac cac cct gat gtc Tyr Asp Tyr Leu Met Tyr Ala Asp Val Asp Tyr Asp His Pro Asp Val 195 200 205			624
gtg gca gag aca aaa aaa tgg ggt atc tgg tat gcg aat gaa ctg tca Val Ala Glu Thr Lys Lys Trp Gly Ile Trp Tyr Ala Asn Glu Leu Ser 210 215 220			672
tta gac ggc ttc cgt att gat gcc gcc aaa cat att aaa ttt tca ttt Leu Asp Gly Phe Arg Ile Asp Ala Ala Lys His Ile Lys Phe Ser Phe 225 230 235 240			720
ctg cgt gat tgg gtt cag gcg gtc aga cag gcg acg gga aaa gaa atg Leu Arg Asp Trp Val Gln Ala Val Arg Gln Ala Thr Gly Lys Glu Met 245 250 255			768
ttt acg gta gct gaa tat tgg cag aat gac ttg ggc gcg ctg gaa aac Phe Thr Val Ala Glu Tyr Trp Gln Asn Asp Leu Gly Ala Leu Glu Asn 260 265 270			816
tat ttg aac aaa aca aat ttt aat cat tca gtg ttt gac gtg ccg ctt Tyr Leu Asn Lys Thr Asn Phe Asn His Ser Val Phe Asp Val Pro Leu 275 280 285			864
cat tat cag ttc cat gct gca tcg aca cag gga ggc ggc tat gat atg His Tyr Gln Phe His Ala Ala Ser Thr Gln Gly Gly Gly Tyr Asp Met 290 295 300			912
agg aaa ttg ctg aac agt acg gtc gtt tcc aag cat ccg ttg aaa gcg Arg Lys Leu Leu Asn Ser Thr Val Val Ser Lys His Pro Leu Lys Ala 305 310 315 320			960
gtt aca ttt gtc gat aac cat gat aca cag ccg ggg caa tcg ctt gag Val Thr Phe Val Asp Asn His Asp Thr Gln Pro Gly Gln Ser Leu Glu 325 330 335			1008
tcg act gtc caa aca tgg ttt aag ccg ctt gct tac gct ttt att ctc Ser Thr Val Gln Thr Trp Phe Lys Pro Leu Ala Tyr Ala Phe Ile Leu 340 345 350			1056
aca agg gaa tct gga tac cct cag gtt ttc tac ggg gat atg tac ggg Thr Arg Glu Ser Gly Tyr Pro Gln Val Phe Tyr Gly Asp Met Tyr Gly 355 360 365			1104
acg aaa gga gac tcc cag cgc gaa att cct gcc ttg aaa cac aaa att Thr Lys Gly Asp Ser Gln Arg Glu Ile Pro Ala Leu Lys His Lys Ile 370 375 380			1152
gaa ccg atc tta aaa gcg aga aaa cag tat gcg tac gga gca cag cat Glu Pro Ile Leu Lys Ala Arg Lys Gln Tyr Ala Tyr Gly Ala Gln His 385 390 400			1200
gat tat ttc gac cac cat gac att gtc ggc tgg aca agg gaa ggc gac Asp Tyr Phe Asp His His Asp Ile Val Gly Trp Thr Arg Glu Gly Asp 1248			

HENK0060.ST25.txt

405	410	415	
agc tcg gtt gca aat tca ggt ttg gcg gca tta ata aca gac gga ccc			1296
Ser Ser Val Ala Asn Ser Gly Leu Ala Ala Leu Ile Thr Asp Gly Pro	420	430	
ggt ggg gca aag cga atg tat gtc ggc cgg caa aac gcc ggt gag aca			1344
Gly Gly Ala Lys Arg Met Tyr Val Gly Arg Gln Asn Ala Gly Glu Thr	440	445	
tgg cat gac att acc gga aac cgt tcg gag ccg gtt gtc atc aat tcg			1392
Trp His Asp Ile Thr Gly Asn Arg Ser Glu Pro Val Val Ile Asn Ser	450	460	
gaa ggc tgg gga gag ttt cac gta aac ggc ggg tcg gtt tca att tat			1440
Glu Gly Trp Gly Glu Phe His Val Asn Gly Gly Ser Val Ser Ile Tyr	470	475	480
ggt caa aga tag			1452
Val Gln Arg			

<210> 12
 <211> 483
 <212> PRT
 <213> Artificial

<220>
 <223> Synthetic Construct

<400> 12

Val Asn Gly Thr Leu Met Gln Tyr Phe Glu Trp Tyr Thr Pro Asn Asp	1	5	10	15
Gly Gln His Trp Lys Arg Leu Gln Asn Asp Ala Glu His Leu Ser Asp	20	25	30	
Ile Gly Ile Thr Ala Val Trp Ile Pro Pro Ala Tyr Lys Gly Leu Ser	35	40	45	
Gln Ser Asp Asn Gly Tyr Gly Pro Tyr Asp Leu Tyr Asp Leu Gly Glu	50	55	60	
Phe Gln Gln Lys Gly Thr Val Arg Thr Lys Tyr Gly Thr Lys Ser Glu	65	70	75	80
Leu Gln Asp Ala Ile Gly Ser Leu His Ser Arg Asn Val Gln Val Tyr	85	90	95	
Gly Asp Val Val Leu Asn His Lys Ala Gly Ala Asp Ala Thr Glu Asp	100	105	110	
Val Thr Ala Val Glu Val Asn Pro Ala Asn Arg Asn Gln Glu Thr Ser	115	120	125	
Glu Glu Tyr Gln Ile Lys Ala Trp Thr Asp Phe Arg Phe Pro Gly Arg	130	135	140	

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Gly Asn Thr Tyr Ser Asp Phe Lys Trp His Trp Tyr His Phe Asp Gly
 145 150 155 160
 Ala Asp Trp Asp Glu Ser Arg Lys Ile Ser Arg Ile Phe Lys Phe Arg
 165 170 175
 Gly Glu Gly Lys Ala Trp Asp Trp Glu Val Ser Ser Glu Asn Gly Asn
 180 185 190
 Tyr Asp Tyr Leu Met Tyr Ala Asp Val Asp Tyr Asp His Pro Asp Val
 195 200 205
 Val Ala Glu Thr Lys Lys Trp Gly Ile Trp Tyr Ala Asn Glu Leu Ser
 210 215 220
 Leu Asp Gly Phe Arg Ile Asp Ala Ala Lys His Ile Lys Phe Ser Phe
 225 230 235 240
 Leu Arg Asp Trp Val Gln Ala Val Arg Gln Ala Thr Gly Lys Glu Met
 245 250 255
 Phe Thr Val Ala Glu Tyr Trp Gln Asn Asp Leu Gly Ala Leu Glu Asn
 260 265 270
 Tyr Leu Asn Lys Thr Asn Phe Asn His Ser Val Phe Asp Val Pro Leu
 275 280 285
 His Tyr Gln Phe His Ala Ala Ser Thr Gln Gly Gly Gly Tyr Asp Met
 290 295 300
 Arg Lys Leu Leu Asn Ser Thr Val Val Ser Lys His Pro Leu Lys Ala
 305 310 315 320
 Val Thr Phe Val Asp Asn His Asp Thr Gln Pro Gly Gln Ser Leu Glu
 325 330 335
 Ser Thr Val Gln Thr Trp Phe Lys Pro Leu Ala Tyr Ala Phe Ile Leu
 340 345 350
 Thr Arg Glu Ser Gly Tyr Pro Gln Val Phe Tyr Gly Asp Met Tyr Gly
 355 360 365
 Thr Lys Gly Asp Ser Gln Arg Glu Ile Pro Ala Leu Lys His Lys Ile
 370 375 380
 Glu Pro Ile Leu Lys Ala Arg Lys Gln Tyr Ala Tyr Gly Ala Gln His
 385 390 395 400
 Asp Tyr Phe Asp His His Asp Ile Val Gly Trp Thr Arg Glu Gly Asp
 405 410 415

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Ser Ser Val Ala Asn Ser Gly Leu Ala Ala Leu Ile Thr Asp Gly Pro
420 425 430

Gly Gly Ala Lys Arg Met Tyr Val Gly Arg Gln Asn Ala Gly Glu Thr
435 440 445

Trp His Asp Ile Thr Gly Asn Arg Ser Glu Pro Val Val Ile Asn Ser
450 455 460

Glu Gly Trp Gly Glu Phe His Val Asn Gly Gly Ser Val Ser Ile Tyr
465 470 475 480

Val Gln Arg

<210> 13
<211> 1452
<212> DNA
<213> Artificial

<220>
<223> Fusion of Alpha-Amylase-Gene von B. licheniformis and B. amyloliquefaciens (ALA34-84)

<220>
<221> CDS
<222> (1)..(1449)

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ggc cag cat tgg aaa cga ttg cag aat gat gcg gaa cat tta tcg gat 96
Gly Gln His Trp Lys Arg Leu Gln Asn Asp Ala Glu His Leu Ser Asp
20 25 30
atc ggt att act gcc gtc tgg att ccc ccg gca tat aag gga acg agc 144
Ile Gly Ile Thr Ala Val Trp Ile Pro Pro Ala Tyr Lys Gly Thr Ser
35 40 45
caa gcg gat gtg ggc tac ggt gct tac gac ctt tat gat tta ggg gag 192
Gln Ala Asp Val Gly Tyr Gly Ala Tyr Asp Leu Tyr Asp Leu Gly Glu
50 55 60
ttt cat caa aaa ggg acg gtt cgg aca aag tac ggc aca aaa gga gag 240
Phe His Gln Lys Gly Thr Val Arg Thr Lys Tyr Gly Thr Lys Gly Glu
65 70 75 80
ctg caa tct gcg atc ggc tca ctg cat tcc cgg aac gtc caa gta tac 288
Leu Gln Ser Ala Ile Gly Ser Leu His Ser Arg Asn Val Gln Val Tyr
85 90 95
gga gat gtg gtt ttg aat cat aag gct ggt gct gat gca aca gaa gat 336
Gly Asp Val Val Leu Asn His Lys Ala Gly Ala Asp Ala Thr Glu Asp
100 105 110
gta act gcc gtc gaa gtc aat ccg gcc aat aga aat cag gaa act tcg 384
Val Thr Ala Val Glu Val Asn Pro Ala Asn Arg Asn Gln Glu Thr Ser
115 120 125

HENK0060.ST25.txt

gag Glu	gaa Glu 130	tat Tyr	caa Gln	atc Ile	aaa Lys	gcg Ala 135	tgg Trp	acg Thr	gat Asp	ttt Phe	cgt Arg 140	ttt Phe	ccg Pro	ggc Gly	cgt Arg	432
gga Gly 145	aac Asn	acg Thr	tac Tyr	agt Ser	gat Asp 150	ttt Phe	aaa Lys	tgg Trp	cat His	tgg Trp 155	tat Tyr	cat His	ttc Phe	gac Asp	gga Gly 160	480
gcg Ala	gac Asp	tgg Trp	gat Asp	gaa Glu 165	tcc Ser	cgg Arg	aag Lys	atc Ile	agc Ser 170	cgc Arg	atc Ile	ttt Phe	aag Lys	ttt Phe 175	cgt Arg	528
ggg Gly	gaa Glu	gga Gly	aaa Lys 180	gcg Ala	tgg Trp	gat Asp	tgg Trp	gaa Glu 185	gta Val	tca Ser	agt Ser	gaa Glu	aac Asn 190	ggc Gly	aac Asn	576
tat Tyr	gac Asp	tat Tyr 195	tta Leu	atg Met	tat Tyr	gct Ala	gat Asp 200	gtt Val	gac Asp	tac Tyr	gac Asp	cac His 205	cct Pro	gat Asp	gtc Val	624
gtg Val	gca Ala 210	gag Glu	aca Thr	aaa Lys	aaa Lys	tgg Trp 215	ggt Gly	atc Ile	tgg Trp	tat Tyr	gcg Ala 220	aat Asn	gaa Glu	ctg Leu	tca Ser	672
tta Leu 225	gac Asp	ggc Gly	ttc Phe	cgt Arg	att Ile 230	gat Asp	gcc Ala	gcc Ala	aaa Lys	cat His 235	att Ile	aaa Lys	ttt Phe	tca Ser	ttt Phe 240	720
ctg Leu	cgt Arg	gat Asp	tgg Trp	gtt Val 245	cag Gln	gcg Ala	gtc Val	aga Arg	cag Gln 250	gcg Ala	acg Thr	gga Gly	aaa Lys	gaa Glu 255	atg Met	768
ttt Phe	acg Thr	gtt Val	gcg Ala 260	gag Glu	tat Tyr	tgg Trp	cag Gln	aat Asn 265	aat Asn	gcc Ala	ggg Gly	aaa Lys	ctc Leu 270	gaa Glu	aac Asn	816
tac Tyr	ttg Leu	aat Asn 275	aaa Lys	aca Thr	agc Ser	ttt Phe	aat Asn 280	caa Gln	tcc Ser	gtg Val	ttt Phe	gat Asp 285	gtt Val	ccg Pro	ctt Leu	864
cat His	ttc Phe 290	aat Asn	tta Leu	cag Gln	gcg Ala	gct Ala 295	tcc Ser	tca Ser	caa Gln	gga Gly	ggc Gly 300	gga Gly	tat Tyr	gat Asp	atg Met	912
agg Arg 305	cgt Arg	ttg Leu	ctg Leu	gac Asp	ggt Gly 310	acc Thr	gtt Val	gtg Val	tcc Ser	agg Arg 315	cat His	ccg Pro	gaa Glu	aag Lys	gcg Ala 320	960
gtt Val	aca Thr	ttt Phe	gtt Val	gaa Glu 325	aat Asn	cat His	gac Asp	aca Thr	cag Gln 330	ccg Pro	gga Gly	cag Gln	tca Ser	ttg Leu 335	gaa Glu	1008
tcg Ser	aca Thr	gtc Val	caa Gln 340	act Thr	tgg Trp	ttt Phe	aaa Lys	ccg Pro 345	ctt Leu	gca Ala	tac Tyr	gcc Ala 350	ttt Phe 350	att Ile	ttg Leu	1056
aca Thr	aga Arg	gaa Glu 355	tcc Ser	ggt Gly	tat Tyr	cct Pro	cag Gln 360	gtg Val	ttc Phe	tat Tyr	ggg Gly	gat Asp 365	atg Met	tac Tyr	ggg Gly	1104
aca Thr	aaa Lys 370	ggg Gly	aca Thr	tcg Ser	cca Pro	aag Lys 375	gaa Glu	att Ile	ccc Pro	tca Ser	ctg Leu 380	aaa Lys	gat Asp	aat Asn	ata Ile	1152
gag Glu 385	ccg Pro	att Ile	tta Leu	aaa Lys	gcg Ala 390	cgt Arg	aag Lys	gag Glu	tac Tyr	gca Ala 395	tac Tyr	ggg Gly	ccc Pro	cag Gln	cac His 400	1200

HENK0060.ST25.txt

gat	tat	att	gac	cac	ccg	gat	gtg	atc	gga	tgg	acg	agg	gaa	ggt	gac	1248
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				405					410					415		
agc	tcc	gcc	gcc	aaa	tca	ggt	ttg	gcc	gct	tta	atc	acg	gac	gga	ccc	1296
Ser	Ser	Ala	Ala	Lys	Ser	Gly	Leu	Ala	Ala	Leu	Ile	Thr	Asp	Gly	Pro	
			420					425					430			
ggc	gga	tca	aag	cgg	atg	tat	gcc	ggc	ctg	aaa	aat	gcc	ggc	gag	aca	1344
Gly	Gly	Ser	Lys	Arg	Met	Tyr	Ala	Gly	Leu	Lys	Asn	Ala	Gly	Glu	Thr	
		435					440					445				
tgg	tat	gac	ata	acg	ggc	aac	cgt	tca	gat	act	gta	aaa	atc	gga	tct	1392
Trp	Tyr	Asp	Ile	Thr	Gly	Asn	Arg	Ser	Asp	Thr	Val	Lys	Ile	Gly	Ser	
	450					455					460					
gac	ggc	tgg	gga	gag	ttt	cat	gta	aac	gat	ggg	tcc	gtc	tcc	att	tat	1440
Asp	Gly	Trp	Gly	Glu	Phe	His	Val	Asn	Asp	Gly	Ser	Val	Ser	Ile	Tyr	
465					470					475					480	
ggt	cag	aaa	taa													1452
Val	Gln	Lys														

<210> 14
 <211> 483
 <212> PRT
 <213> Artificial

<220>
 <223> Synthetic Construct

<400> 14

Val	Asn	Gly	Thr	Leu	Met	Gln	Tyr	Phe	Glu	Trp	Tyr	Thr	Pro	Asn	Asp	
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Gly	Gln	His	Trp	Lys	Arg	Leu	Gln	Asn	Asp	Ala	Glu	His	Leu	Ser	Asp	
		20					25						30			
Ile	Gly	Ile	Thr	Ala	Val	Trp	Ile	Pro	Pro	Ala	Tyr	Lys	Gly	Thr	Ser	
	35						40					45				
Gln	Ala	Asp	Val	Gly	Tyr	Gly	Ala	Tyr	Asp	Leu	Tyr	Asp	Leu	Gly	Glu	
	50					55				60						
Phe	His	Gln	Lys	Gly	Thr	Val	Arg	Thr	Lys	Tyr	Gly	Thr	Lys	Gly	Glu	
65					70					75					80	
Leu	Gln	Ser	Ala	Ile	Gly	Ser	Leu	His	Ser	Arg	Asn	Val	Gln	Val	Tyr	
				85					90					95		
Gly	Asp	Val	Val	Leu	Asn	His	Lys	Ala	Gly	Ala	Asp	Ala	Thr	Glu	Asp	
		100						105					110			
Val	Thr	Ala	Val	Glu	Val	Asn	Pro	Ala	Asn	Arg	Asn	Gln	Glu	Thr	Ser	
	115						120					125				
Glu	Glu	Tyr	Gln	Ile	Lys	Ala	Trp	Thr	Asp	Phe	Arg	Phe	Pro	Gly	Arg	

130

135

140

Gly Asn Thr Tyr Ser Asp Phe Lys Trp His Trp Tyr His Phe Asp Gly
 145 150 155 160

Ala Asp Trp Asp Glu Ser Arg Lys Ile Ser Arg Ile Phe Lys Phe Arg
 165 170 175

Gly Glu Gly Lys Ala Trp Asp Trp Glu Val Ser Ser Glu Asn Gly Asn
 180 185 190

Tyr Asp Tyr Leu Met Tyr Ala Asp Val Asp Tyr Asp His Pro Asp Val
 195 200 205

Val Ala Glu Thr Lys Lys Trp Gly Ile Trp Tyr Ala Asn Glu Leu Ser
 210 215 220

Leu Asp Gly Phe Arg Ile Asp Ala Ala Lys His Ile Lys Phe Ser Phe
 225 230 235 240

Leu Arg Asp Trp Val Gln Ala Val Arg Gln Ala Thr Gly Lys Glu Met
 245 250 255

Phe Thr Val Ala Glu Tyr Trp Gln Asn Asn Ala Gly Lys Leu Glu Asn
 260 265 270

Tyr Leu Asn Lys Thr Ser Phe Asn Gln Ser Val Phe Asp Val Pro Leu
 275 280 285

His Phe Asn Leu Gln Ala Ala Ser Ser Gln Gly Gly Gly Tyr Asp Met
 290 295 300

Arg Arg Leu Leu Asp Gly Thr Val Val Ser Arg His Pro Glu Lys Ala
 305 310 315 320

Val Thr Phe Val Glu Asn His Asp Thr Gln Pro Gly Gln Ser Leu Glu
 325 330 335

Ser Thr Val Gln Thr Trp Phe Lys Pro Leu Ala Tyr Ala Phe Ile Leu
 340 345 350

Thr Arg Glu Ser Gly Tyr Pro Gln Val Phe Tyr Gly Asp Met Tyr Gly
 355 360 365

Thr Lys Gly Thr Ser Pro Lys Glu Ile Pro Ser Leu Lys Asp Asn Ile
 370 375 380

Glu Pro Ile Leu Lys Ala Arg Lys Glu Tyr Ala Tyr Gly Pro Gln His
 385 390 395 400

Asp Tyr Ile Asp His Pro Asp Val Ile Gly Trp Thr Arg Glu Gly Asp
 Page 28

Ser Ser Ala Ala Lys Ser Gly Leu Ala Ala Leu Ile Thr Asp Gly Pro
420 425 430

Gly Gly Ser Lys Arg Met Tyr Ala Gly Leu Lys Asn Ala Gly Glu Thr
435 440 445

Trp Tyr Asp Ile Thr Gly Asn Arg Ser Asp Thr Val Lys Ile Gly Ser
450 455 460

Asp Gly Trp Gly Glu Phe His Val Asn Asp Gly Ser Val Ser Ile Tyr
465 470 475 480

Val Gln Lys

<210> 15
<211> 1458
<212> DNA
<213> Artificial

<220>
<223> Fusion of Alpha-Amylase-Gene von B. licheniformis and B. amyloliquefaciens (LAL19-433)

<220>
<221> CDS
<222> (1)..(1455)

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aat gac ggc cag cat tgg aaa cga ttg cag aat gat gcg gaa cat tta 96
Asn Asp Gly Gln His Trp Lys Arg Leu Gln Asn Asp Ala Glu His Leu
20 25 30

tcg gat atc gga atc act gcc gtc tgg att cct ccc gca tac aaa gga 144
Ser Asp Ile Gly Ile Thr Ala Val Trp Ile Pro Pro Ala Tyr Lys Gly
35 40 45

ttg agc caa tcc gat aac gga tac gga cct tat gat ttg tat gat tta 192
Leu Ser Gln Ser Asp Asn Gly Tyr Gly Pro Tyr Asp Leu Tyr Asp Leu
50 55 60

gga gaa ttc cag caa aaa ggg acg gtc aga acg aaa tac ggc aca aaa 240
Gly Glu Phe Gln Gln Lys Gly Thr Val Arg Thr Lys Tyr Gly Thr Lys
65 70 75 80

tca gag ctt caa gat gcg atc ggc tca ctg cat tcc cgg aac gtc caa 288
Ser Glu Leu Gln Asp Ala Ile Gly Ser Leu His Ser Arg Asn Val Gln
85 90 95

gta tac gga gat gtg gtt ttg aat cat aag gct ggt gct gat gca aca 336
Val Tyr Gly Asp Val Val Leu Asn His Lys Ala Gly Ala Asp Ala Thr
100 105 110

gaa gat gta act gcc gtc gaa gtc aat ccg gcc aat aga aat cag gaa 384
Glu Asp Val Thr Ala Val Glu Val Asn Pro Ala Asn Arg Asn Gln Glu
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115					120					125						
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Thr	Ser	Glu	Glu	Tyr	Gln	Ile	Lys	Ala	Trp	Thr	Asp	Phe	Arg	Phe	Pro	
	130					135					140					
ggc	cgt	gga	aac	acg	tac	agt	gat	ttt	aaa	tgg	cat	tgg	tat	cat	ttc	480
Gly	Arg	Gly	Asn	Thr	Tyr	Ser	Asp	Phe	Lys	Trp	His	Trp	Tyr	His	Phe	
145					150					155					160	
gac	gga	gcg	gac	tgg	gat	gaa	tcc	cgg	aag	atc	agc	cgc	atc	ttt	aag	528
Asp	Gly	Ala	Asp	Trp	Asp	Glu	Ser	Arg	Lys	Ile	Ser	Arg	Ile	Phe	Lys	
				165					170					175		
ttt	cgt	ggg	gaa	gga	aaa	gcg	tgg	gat	tgg	gaa	gta	tca	agt	gaa	aac	576
Phe	Arg	Gly	Glu	Gly	Lys	Ala	Trp	Asp	Trp	Glu	Val	Ser	Ser	Glu	Asn	
			180					185					190			
ggc	aac	tat	gac	tat	tta	atg	tat	gct	gat	ggt	gac	tac	gac	cac	cct	624
Gly	Asn	Tyr	Asp	Tyr	Leu	Met	Tyr	Ala	Asp	Val	Asp	Tyr	Asp	His	Pro	
		195					200					205				
gat	gtc	gtg	gca	gag	aca	aaa	aaa	tgg	ggt	atc	tgg	tat	gcg	aat	gaa	672
Asp	Val	Val	Ala	Glu	Thr	Lys	Lys	Trp	Gly	Ile	Trp	Tyr	Ala	Asn	Glu	
	210					215					220					
ctg	tca	tta	gac	ggc	ttc	cgt	att	gat	gcc	gcc	aaa	cat	att	aaa	ttt	720
Leu	Ser	Leu	Asp	Gly	Phe	Arg	Ile	Asp	Ala	Ala	Lys	His	Ile	Lys	Phe	
225					230				235						240	
tca	ttt	ctg	cgt	gat	tgg	gtt	cag	gcg	gtc	aga	cag	gcg	acg	gga	aaa	768
Ser	Phe	Leu	Arg	Asp	Trp	Val	Gln	Ala	Val	Arg	Gln	Ala	Thr	Gly	Lys	
				245					250					255		
gaa	atg	ttt	acg	gtt	gcg	gag	tat	tgg	cag	aat	aat	gcc	ggg	aaa	ctc	816
Glu	Met	Phe	Thr	Val	Ala	Glu	Tyr	Trp	Gln	Asn	Asn	Ala	Gly	Lys	Leu	
			260					265					270			
gaa	aac	tac	ttg	aat	aaa	aca	agc	ttt	aat	caa	tcc	gtg	ttt	gat	gtt	864
Glu	Asn	Tyr	Leu	Asn	Lys	Thr	Ser	Phe	Asn	Gln	Ser	Val	Phe	Asp	Val	
		275					280					285				
ccg	ctt	cat	ttc	aat	tta	cag	gcg	gct	tcc	tca	caa	gga	ggc	gga	tat	912
Pro	Leu	His	Phe	Asn	Leu	Gln	Ala	Ala	Ser	Ser	Gln	Gly	Gly	Gly	Tyr	
	290					295					300					
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Asp	Met	Arg	Arg	Leu	Leu	Asp	Gly	Thr	Val	Val	Ser	Arg	His	Pro	Glu	
305					310					315					320	
aag	gcg	gtt	aca	ttt	gtt	gaa	aat	cat	gac	aca	cag	ccg	gga	cag	tca	1008
Lys	Ala	Val	Thr	Phe	Val	Glu	Asn	His	Asp	Thr	Gln	Pro	Gly	Gln	Ser	
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ttg	gaa	tcg	aca	gtc	caa	act	tgg	ttt	aaa	ccg	ctt	gca	tac	gcc	ttt	1056
Leu	Glu	Ser	Thr	Val	Gln	Thr	Trp	Phe	Lys	Pro	Leu	Ala	Tyr	Ala	Phe	
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Ile	Leu	Thr	Arg	Glu	Ser	Gly	Tyr	Pro	Gln	Val	Phe	Tyr	Gly	Asp	Met	
		355					360					365				
tac	ggg	aca	aaa	ggg	aca	tcg	cca	aag	gaa	att	ccc	tca	ctg	aaa	gat	1152
Tyr	Gly	Thr	Lys	Gly	Thr	Ser	Pro	Lys	Glu	Ile	Pro	Ser	Leu	Lys	Asp	
	370					375					380					
aat	ata	gag	ccg	att	tta	aaa	gcg	cgt	aag	gag	tac	gca	tac	ggg	ccc	1200
Asn	Ile	Glu	Pro	Ile	Leu	Lys	Ala	Arg	Lys	Glu	Tyr	Ala	Tyr	Gly	Pro	

HENK0060.ST25.txt

385		390	395	400												
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				405					410					415		
ggt	gac	agc	tcc	gcc	gcc	aaa	tca	ggt	ttg	gcc	gct	tta	atc	acg	gac	1296
Gly	Asp	Ser	Ser	Ala	Ala	Lys	Ser	Gly	Leu	Ala	Ala	Leu	Ile	Thr	Asp	
			420					425					430			
gga	ccc	ggt	ggg	gca	aag	cga	atg	tat	gtc	ggc	cgg	caa	aac	gcc	ggt	1344
Gly	Pro	Gly	Gly	Ala	Lys	Arg	Met	Tyr	Val	Gly	Arg	Gln	Asn	Ala	Gly	
			435				440					445				
gag	aca	tgg	cat	gac	att	acc	gga	aac	cgt	tcg	gag	ccg	gtt	gtc	atc	1392
Glu	Thr	Trp	His	Asp	Ile	Thr	Gly	Asn	Arg	Ser	Glu	Pro	Val	Val	Ile	
	450					455					460					
aat	tcg	gaa	ggc	tgg	gga	gag	ttt	cac	gta	aac	ggc	ggg	tcg	gtt	tca	1440
Asn	Ser	Glu	Gly	Trp	Gly	Glu	Phe	His	Val	Asn	Gly	Gly	Ser	Val	Ser	
					470					475					480	
att	tat	gtt	caa	aga	tag											1458
Ile	Tyr	Val	Gln	Arg												
				485												

<210> 16
 <211> 485
 <212> PRT
 <213> Artificial

<220>
 <223> Synthetic Construct

<400> 16

Ala	Asn	Leu	Asn	Gly	Thr	Leu	Met	Gln	Tyr	Phe	Glu	Trp	Tyr	Met	Pro
1				5					10					15	
Asn	Asp	Gly	Gln	His	Trp	Lys	Arg	Leu	Gln	Asn	Asp	Ala	Glu	His	Leu
			20					25					30		
Ser	Asp	Ile	Gly	Ile	Thr	Ala	Val	Trp	Ile	Pro	Pro	Ala	Tyr	Lys	Gly
		35					40					45			
Leu	Ser	Gln	Ser	Asp	Asn	Gly	Tyr	Gly	Pro	Tyr	Asp	Leu	Tyr	Asp	Leu
	50					55					60				
Gly	Glu	Phe	Gln	Gln	Lys	Gly	Thr	Val	Arg	Thr	Lys	Tyr	Gly	Thr	Lys
65					70				75						80
Ser	Glu	Leu	Gln	Asp	Ala	Ile	Gly	Ser	Leu	His	Ser	Arg	Asn	Val	Gln
				85					90					95	
Val	Tyr	Gly	Asp	Val	Val	Leu	Asn	His	Lys	Ala	Gly	Ala	Asp	Ala	Thr
			100					105					110		
Glu	Asp	Val	Thr	Ala	Val	Glu	Val	Asn	Pro	Ala	Asn	Arg	Asn	Gln	Glu
		115					120					125			

HENK0060.ST25.txt

Thr Ser Glu Glu Tyr Gln Ile Lys Ala Trp Thr Asp Phe Arg Phe Pro
 130 135 140
 Gly Arg Gly Asn Thr Tyr Ser Asp Phe Lys Trp His Trp Tyr His Phe
 145 150 155 160
 Asp Gly Ala Asp Trp Asp Glu Ser Arg Lys Ile Ser Arg Ile Phe Lys
 165 170 175
 Phe Arg Gly Glu Gly Lys Ala Trp Asp Trp Glu Val Ser Ser Glu Asn
 180 185 190
 Gly Asn Tyr Asp Tyr Leu Met Tyr Ala Asp Val Asp Tyr Asp His Pro
 195 200 205
 Asp Val Val Ala Glu Thr Lys Lys Trp Gly Ile Trp Tyr Ala Asn Glu
 210 215 220
 Leu Ser Leu Asp Gly Phe Arg Ile Asp Ala Ala Lys His Ile Lys Phe
 225 230 235 240
 Ser Phe Leu Arg Asp Trp Val Gln Ala Val Arg Gln Ala Thr Gly Lys
 245 250 255
 Glu Met Phe Thr Val Ala Glu Tyr Trp Gln Asn Asn Ala Gly Lys Leu
 260 265 270
 Glu Asn Tyr Leu Asn Lys Thr Ser Phe Asn Gln Ser Val Phe Asp Val
 275 280 285
 Pro Leu His Phe Asn Leu Gln Ala Ala Ser Ser Gln Gly Gly Gly Tyr
 290 295 300
 Asp Met Arg Arg Leu Leu Asp Gly Thr Val Val Ser Arg His Pro Glu
 305 310 315 320
 Lys Ala Val Thr Phe Val Glu Asn His Asp Thr Gln Pro Gly Gln Ser
 325 330 335
 Leu Glu Ser Thr Val Gln Thr Trp Phe Lys Pro Leu Ala Tyr Ala Phe
 340 345 350
 Ile Leu Thr Arg Glu Ser Gly Tyr Pro Gln Val Phe Tyr Gly Asp Met
 355 360 365
 Tyr Gly Thr Lys Gly Thr Ser Pro Lys Glu Ile Pro Ser Leu Lys Asp
 370 375 380
 Asn Ile Glu Pro Ile Leu Lys Ala Arg Lys Glu Tyr Ala Tyr Gly Pro
 385 390 395 400

HENK0060.ST25.txt

Gln His Asp Tyr Ile Asp His Pro Asp Val Ile Gly Trp Thr Arg Glu
405 410 415

Gly Asp Ser Ser Ala Ala Lys Ser Gly Leu Ala Ala Leu Ile Thr Asp
420 425 430

Gly Pro Gly Gly Ala Lys Arg Met Tyr Val Gly Arg Gln Asn Ala Gly
435 440 445

Glu Thr Trp His Asp Ile Thr Gly Asn Arg Ser Glu Pro Val Val Ile
450 455 460

Asn Ser Glu Gly Trp Gly Glu Phe His Val Asn Gly Gly Ser Val Ser
465 470 475 480

Ile Tyr Val Gln Arg
485

<210> 17
<211> 1452
<212> DNA
<213> Artificial

<220>
<223> Fusion of Alpha-Amylase-Gene von B. licheniformis and B. amyloliquefaciens (LAL19-153)

<220>
<221> CDS
<222> (1)..(1449)

<400> 17
gca aat ctt aat ggg acg ctg atg cag tat ttt gaa tgg tac atg ccc 48
Ala Asn Leu Asn Gly Thr Leu Met Gln Tyr Phe Glu Trp Tyr Met Pro
1 5 10 15

aat gac ggc cag cat tgg aaa cga ttg cag aat gat gcg gaa cat tta 96
Asn Asp Gly Gln His Trp Lys Arg Leu Gln Asn Asp Ala Glu His Leu
20 25 30

tcg gat atc gga atc act gcc gtc tgg att cct ccc gca tac aaa gga 144
Ser Asp Ile Gly Ile Thr Ala Val Trp Ile Pro Pro Ala Tyr Lys Gly
35 40 45

ttg agc caa tcc gat aac gga tac gga cct tat gat ttg tat gat tta 192
Leu Ser Gln Ser Asp Asn Gly Tyr Gly Pro Tyr Asp Leu Tyr Asp Leu
50 55 60

gga gaa ttc cag caa aaa ggg acg gtc aga acg aaa tac ggc aca aaa 240
Gly Glu Phe Gln Gln Lys Gly Thr Val Arg Thr Lys Tyr Gly Thr Lys
65 70 75 80

tca gag ctt caa gat gcg atc ggc tca ctg cat tcc cgg aac gtc caa 288
Ser Glu Leu Gln Asp Ala Ile Gly Ser Leu His Ser Arg Asn Val Gln
85 90 95

gta tac gga gat gtg gtt ttg aat cat aag gct ggt gct gat gca aca 336
Val Tyr Gly Asp Val Val Leu Asn His Lys Ala Gly Ala Asp Ala Thr
100 105 110

HENK0060.ST25.txt

gaa gat gta act gcc gtc gaa gtc	aat ccg gcc aat aga aat cag gaa	384
Glu Asp Val Thr Ala Val Glu Val	Asn Pro Ala Asn Arg Asn Gln Glu	
115	120 125	
act tcg gag gaa tat caa atc aaa gcg tgg acg gat ttt cgt ttt ccg	432	
Thr Ser Glu Glu Tyr Gln Ile Lys Ala Trp Thr Asp Phe Arg Phe Pro		
130	135 140	
ggc cgt gga aac acg tac agt gat ttt aaa tgg cat tgg tac cat ttt	480	
Gly Arg Gly Asn Thr Tyr Ser Asp Phe Lys Trp His Trp Tyr His Phe		
145	150 155 160	
gac gga acc gat tgg gac gag tcc cga aag ctg aac cgc atc tat aag	528	
Asp Gly Thr Asp Trp Asp Glu Ser Arg Lys Leu Asn Arg Ile Tyr Lys		
165	170 175	
ttt caa gga aag gct tgg gat tgg gaa gtt tcc aat gaa aac ggc aac	576	
Phe Gln Gly Lys Ala Trp Asp Trp Glu Val Ser Asn Glu Asn Gly Asn		
180	185 190	
tat gat tat ttg atg tat gcc gac atc gat tat gac cat cct gat gtc	624	
Tyr Asp Tyr Leu Met Tyr Ala Asp Ile Asp Tyr Asp His Pro Asp Val		
195	200 205	
gca gca gaa att aag aga tgg ggc act tgg tat gcc aat gaa ctg caa	672	
Ala Ala Glu Ile Lys Arg Trp Gly Thr Trp Tyr Ala Asn Glu Leu Gln		
210	215 220	
ttg gac ggt ttc cgt ctt gat gct gtc aaa cac att aaa ttt tct ttt	720	
Leu Asp Gly Phe Arg Leu Asp Ala Val Lys His Ile Lys Phe Ser Phe		
225	230 235 240	
ttg cgg gat tgg gtt aat cat gtc agg gaa aaa acg ggg aag gaa atg	768	
Leu Arg Asp Trp Val Asn His Val Arg Glu Lys Thr Gly Lys Glu Met		
245	250 255	
ttt acg gta gct gaa tat tgg cag aat gac ttg ggc gcg ctg gaa aac	816	
Phe Thr Val Ala Glu Tyr Trp Gln Asn Asp Leu Gly Ala Leu Glu Asn		
260	265 270	
tat ttg aac aaa aca aat ttt aat cat tca gtg ttt gac gtg ccg ctt	864	
Tyr Leu Asn Lys Thr Asn Phe Asn His Ser Val Phe Asp Val Pro Leu		
275	280 285	
cat tat cag ttc cat gct gca tcg aca cag gga ggc ggc tat gat atg	912	
His Tyr Gln Phe His Ala Ala Ser Thr Gln Gly Gly Gly Tyr Asp Met		
290	295 300	
agg aaa ttg ctg aac agt acg gtc gtt tcc aag cat ccg ttg aaa gcg	960	
Arg Lys Leu Leu Asn Ser Thr Val Val Ser Lys His Pro Leu Lys Ala		
305	310 315 320	
gtt aca ttt gtc gat aac cat gat aca cag ccg ggg caa tcg ctt gag	1008	
Val Thr Phe Val Asp Asn His Asp Thr Gln Pro Gly Gln Ser Leu Glu		
325	330 335	
tcg act gtc caa aca tgg ttt aag ccg ctt gct tac gct ttt att ctc	1056	
Ser Thr Val Gln Thr Trp Phe Lys Pro Leu Ala Tyr Ala Phe Ile Leu		
340	345 350	
aca agg gaa tct gga tac cct cag gtt ttc tac ggg gat atg tac ggg	1104	
Thr Arg Glu Ser Gly Tyr Pro Gln Val Phe Tyr Gly Asp Met Tyr Gly		
355	360 365	
acg aaa gga gac tcc cag cgc gaa att cct gcc ttg aaa cac aaa att	1152	
Thr Lys Gly Asp Ser Gln Arg Glu Ile Pro Ala Leu Lys His Lys Ile		
370	375 380	

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gaa ccg atc tta aaa gcg aga aaa cag tat gcg tac gga gca cag cat	1200
Glu Pro Ile Leu Lys Ala Arg Lys Gln Tyr Ala Tyr Gly Ala Gln His	
385 390 395 400	
gat tat ttc gac cac cat gac att gtc ggc tgg aca agg gaa ggc gac	1248
Asp Tyr Phe Asp His His Asp Ile Val Gly Trp Thr Arg Glu Gly Asp	
405 410 415	
agc tcg gtt gca aat tca ggt ttg gcg gca tta ata aca gac gga ccc	1296
Ser Ser Val Ala Asn Ser Gly Leu Ala Ala Leu Ile Thr Asp Gly Pro	
420 425 430	
ggt ggg gca aag cga atg tat gtc ggc cgg caa aac gcc ggt gag aca	1344
Gly Gly Ala Lys Arg Met Tyr Val Gly Arg Gln Asn Ala Gly Glu Thr	
435 440 445	
tgg cat gac att acc gga aac cgt tcg gag ccg gtt gtc atc aat tcg	1392
Trp His Asp Ile Thr Gly Asn Arg Ser Glu Pro Val Val Ile Asn Ser	
450 455 460	
gaa ggc tgg gga gag ttt cac gta aac ggc ggg tcg gtt tca att tat	1440
Glu Gly Trp Gly Glu Phe His Val Asn Gly Gly Ser Val Ser Ile Tyr	
465 470 475 480	
ggt caa aga tag	1452
Val Gln Arg	

<210> 18
 <211> 483
 <212> PRT
 <213> Artificial

<220>
 <223> Synthetic Construct

<400> 18

Ala Asn Leu Asn Gly Thr Leu Met Gln Tyr Phe Glu Trp Tyr Met Pro
1 5 10 15
Asn Asp Gly Gln His Trp Lys Arg Leu Gln Asn Asp Ala Glu His Leu
20 25 30
Ser Asp Ile Gly Ile Thr Ala Val Trp Ile Pro Pro Ala Tyr Lys Gly
35 40 45
Leu Ser Gln Ser Asp Asn Gly Tyr Gly Pro Tyr Asp Leu Tyr Asp Leu
50 55 60
Gly Glu Phe Gln Gln Lys Gly Thr Val Arg Thr Lys Tyr Gly Thr Lys
65 70 75 80
Ser Glu Leu Gln Asp Ala Ile Gly Ser Leu His Ser Arg Asn Val Gln
85 90 95
Val Tyr Gly Asp Val Val Leu Asn His Lys Ala Gly Ala Asp Ala Thr
100 105 110
Glu Asp Val Thr Ala Val Glu Val Asn Pro Ala Asn Arg Asn Gln Glu

115

120

125

Thr Ser Glu Glu Tyr Gln Ile Lys Ala Trp Thr Asp Phe Arg Phe Pro
 130 135 140

Gly Arg Gly Asn Thr Tyr Ser Asp Phe Lys Trp His Trp Tyr His Phe
 145 150 155 160

Asp Gly Thr Asp Trp Asp Glu Ser Arg Lys Leu Asn Arg Ile Tyr Lys
 165 170 175

Phe Gln Gly Lys Ala Trp Asp Trp Glu Val Ser Asn Glu Asn Gly Asn
 180 185 190

Tyr Asp Tyr Leu Met Tyr Ala Asp Ile Asp Tyr Asp His Pro Asp Val
 195 200 205

Ala Ala Glu Ile Lys Arg Trp Gly Thr Trp Tyr Ala Asn Glu Leu Gln
 210 215 220

Leu Asp Gly Phe Arg Leu Asp Ala Val Lys His Ile Lys Phe Ser Phe
 225 230 235 240

Leu Arg Asp Trp Val Asn His Val Arg Glu Lys Thr Gly Lys Glu Met
 245 250 255

Phe Thr Val Ala Glu Tyr Trp Gln Asn Asp Leu Gly Ala Leu Glu Asn
 260 265 270

Tyr Leu Asn Lys Thr Asn Phe Asn His Ser Val Phe Asp Val Pro Leu
 275 280 285

His Tyr Gln Phe His Ala Ala Ser Thr Gln Gly Gly Gly Tyr Asp Met
 290 295 300

Arg Lys Leu Leu Asn Ser Thr Val Val Ser Lys His Pro Leu Lys Ala
 305 310 315 320

Val Thr Phe Val Asp Asn His Asp Thr Gln Pro Gly Gln Ser Leu Glu
 325 330 335

Ser Thr Val Gln Thr Trp Phe Lys Pro Leu Ala Tyr Ala Phe Ile Leu
 340 345 350

Thr Arg Glu Ser Gly Tyr Pro Gln Val Phe Tyr Gly Asp Met Tyr Gly
 355 360 365

Thr Lys Gly Asp Ser Gln Arg Glu Ile Pro Ala Leu Lys His Lys Ile
 370 375 380

Glu Pro Ile Leu Lys Ala Arg Lys Gln Tyr Ala Tyr Gly Ala Gln His
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385 390 395 400

Asp Tyr Phe Asp His His Asp Ile Val Gly Trp Thr Arg Glu Gly Asp
405 410 415

Ser Ser Val Ala Asn Ser Gly Leu Ala Ala Leu Ile Thr Asp Gly Pro
420 425 430

Gly Gly Ala Lys Arg Met Tyr Val Gly Arg Gln Asn Ala Gly Glu Thr
435 440 445

Trp His Asp Ile Thr Gly Asn Arg Ser Glu Pro Val Val Ile Asn Ser
450 455 460

Glu Gly Trp Gly Glu Phe His Val Asn Gly Gly Ser Val Ser Ile Tyr
465 470 475 480

Val Gln Arg

<210> 19
<211> 512
<212> PRT
<213> Bacillus licheniformis

<400> 19

Met Lys Gln Gln Lys Arg Leu Tyr Ala Arg Leu Leu Thr Leu Leu Phe
1 5 10 15

Ala Leu Ile Phe Leu Leu Pro His Ser Ala Ala Ala Ala Ala Asn Leu
20 25 30

Asn Gly Thr Leu Met Gln Tyr Phe Glu Trp Tyr Met Pro Asn Asp Gly
35 40 45

Gln His Trp Lys Arg Leu Gln Asn Asp Ser Ala Tyr Leu Ala Glu His
50 55 60

Gly Ile Thr Ala Val Trp Ile Pro Pro Ala Tyr Lys Gly Thr Ser Gln
65 70 75 80

Ala Asp Val Gly Tyr Gly Ala Tyr Asp Leu Tyr Asp Leu Gly Glu Phe
85 90 95

His Gln Lys Gly Thr Val Arg Thr Lys Tyr Gly Thr Lys Gly Glu Leu
100 105 110

Gln Ser Ala Ile Lys Ser Leu His Ser Arg Asp Ile Asn Val Tyr Gly
115 120 125

Asp Val Val Ile Asn His Lys Gly Gly Ala Asp Ala Thr Glu Asp Val
130 135 140

HENK0060.ST25.txt

Thr Ala Val Glu Val Asp Pro Ala Asp Arg Asn Arg Val Ile Ser Gly
 145 150 155 160
 Glu His Arg Ile Lys Ala Trp Thr His Phe His Phe Pro Gly Arg Gly
 165 170 175
 Ser Thr Tyr Ser Asp Phe Lys Trp His Trp Tyr His Phe Asp Gly Thr
 180 185 190
 Asp Trp Asp Glu Ser Arg Lys Leu Asn Arg Ile Tyr Lys Phe Gln Gly
 195 200 205
 Lys Ala Trp Asp Trp Glu Val Ser Asn Glu Asn Gly Asn Tyr Asp Tyr
 210 215 220
 Leu Met Tyr Ala Asp Ile Asp Tyr Asp His Pro Asp Val Ala Ala Glu
 225 230 235 240
 Ile Lys Arg Trp Gly Thr Trp Tyr Ala Asn Glu Leu Gln Leu Asp Gly
 245 250 255
 Phe Arg Leu Asp Ala Val Lys His Ile Lys Phe Ser Phe Leu Arg Asp
 260 265 270
 Trp Val Asn His Val Arg Glu Lys Thr Gly Lys Glu Met Phe Thr Val
 275 280 285
 Ala Glu Tyr Trp Gln Asn Asp Leu Gly Ala Leu Glu Asn Tyr Leu Asn
 290 295 300
 Lys Thr Asn Phe Asn His Ser Val Phe Asp Val Pro Leu His Tyr Gln
 305 310 315 320
 Phe His Ala Ala Ser Thr Gln Gly Gly Gly Tyr Asp Met Arg Lys Leu
 325 330 335
 Leu Asn Ser Thr Val Val Ser Lys His Pro Leu Lys Ala Val Thr Phe
 340 345 350
 Val Asp Asn His Asp Thr Gln Pro Gly Gln Ser Leu Glu Ser Thr Val
 355 360 365
 Gln Thr Trp Phe Lys Pro Leu Ala Tyr Ala Phe Ile Leu Thr Arg Glu
 370 375 380
 Ser Gly Tyr Pro Gln Val Phe Tyr Gly Asp Met Tyr Gly Thr Lys Gly
 385 390 395 400
 Asp Ser Gln Arg Glu Ile Pro Ala Leu Lys His Lys Ile Glu Pro Ile
 405 410 415

Leu Lys Ala Arg Lys Gln Tyr Ala Tyr Gly Ala Gln His Asp Tyr Phe
420 425 430

Asp His His Asp Ile Val Gly Trp Thr Arg Glu Gly Asp Ser Ser Val
435 440 445

Ala Asn Ser Gly Leu Ala Ala Leu Ile Thr Asp Gly Pro Gly Gly Ala
450 455 460

Lys Arg Met Tyr Val Gly Arg Gln Asn Ala Gly Glu Thr Trp His Asp
465 470 475 480

Ile Thr Gly Asn Arg Ser Glu Pro Val Val Ile Asn Ser Glu Gly Trp
485 490 495

Gly Glu Phe His Val Asn Gly Gly Ser Val Ser Ile Tyr Val Gln Arg
500 505 510

<210> 20
<211> 514
<212> PRT
<213> Bacillus amyloliquefaciens
<400> 20

Met Ile Gln Lys Arg Lys Arg Thr Val Ser Phe Arg Leu Val Leu Met
1 5 10 15

Cys Thr Leu Leu Phe Val Ser Leu Pro Ile Thr Lys Thr Ser Ala Val
20 25 30

Asn Gly Thr Leu Met Gln Tyr Phe Glu Trp Tyr Thr Pro Asn Asp Gly
35 40 45

Gln His Trp Lys Arg Leu Gln Asn Asp Ala Glu His Leu Ser Asp Ile
50 55 60

Gly Ile Thr Ala Val Trp Ile Pro Pro Ala Tyr Lys Gly Leu Ser Gln
65 70 75 80

Ser Asp Asn Gly Tyr Gly Pro Tyr Asp Leu Tyr Asp Leu Gly Glu Phe
85 90 95

Gln Gln Lys Gly Thr Val Arg Thr Lys Tyr Gly Thr Lys Ser Glu Leu
100 105 110

Gln Asp Ala Ile Gly Ser Leu His Ser Arg Asn Val Gln Val Tyr Gly
115 120 125

Asp Val Val Leu Asn His Lys Ala Gly Ala Asp Ala Thr Glu Asp Val
130 135 140

HENK0060.ST25.txt

Thr Ala Val Glu Val Asn Pro Ala Asn Arg Asn Gln Glu Thr Ser Glu
 145 150 155 160
 Glu Tyr Gln Ile Lys Ala Trp Thr Asp Phe Arg Phe Pro Gly Arg Gly
 165 170 175
 Asn Thr Tyr Ser Asp Phe Lys Trp His Trp Tyr His Phe Asp Gly Ala
 180 185 190
 Asp Trp Asp Glu Ser Arg Lys Ile Ser Arg Ile Phe Lys Phe Arg Gly
 195 200 205
 Glu Gly Lys Ala Trp Asp Trp Glu Val Ser Ser Glu Asn Gly Asn Tyr
 210 215 220
 Asp Tyr Leu Met Tyr Ala Asp Val Asp Tyr Asp His Pro Asp Val Val
 225 230 235 240
 Ala Glu Thr Lys Lys Trp Gly Ile Trp Tyr Ala Asn Glu Leu Ser Leu
 245 250 255
 Asp Gly Phe Arg Ile Asp Ala Ala Lys His Ile Lys Phe Ser Phe Leu
 260 265 270
 Arg Asp Trp Val Gln Ala Val Arg Gln Ala Thr Gly Lys Glu Met Phe
 275 280 285
 Thr Val Ala Glu Tyr Trp Gln Asn Asn Ala Gly Lys Leu Glu Asn Tyr
 290 295 300
 Leu Asn Lys Thr Ser Phe Asn Gln Ser Val Phe Asp Val Pro Leu His
 305 310 315 320
 Phe Asn Leu Gln Ala Ala Ser Ser Gln Gly Gly Gly Tyr Asp Met Arg
 325 330 335
 Arg Leu Leu Asp Gly Thr Val Val Ser Arg His Pro Glu Lys Ala Val
 340 345 350
 Thr Phe Val Glu Asn His Asp Thr Gln Pro Gly Gln Ser Leu Glu Ser
 355 360 365
 Thr Val Gln Thr Trp Phe Lys Pro Leu Ala Tyr Ala Phe Ile Leu Thr
 370 375 380
 Arg Glu Ser Gly Tyr Pro Gln Val Phe Tyr Gly Asp Met Tyr Gly Thr
 385 390 395 400
 Lys Gly Thr Ser Pro Lys Glu Ile Pro Ser Leu Lys Asp Asn Ile Glu
 405 410 415

HENK0060.ST25.txt

Pro Ile Leu Lys Ala Arg Lys Glu Tyr Ala Tyr Gly Pro Gln His Asp
420 425 430

Tyr Ile Asp His Pro Asp Val Ile Gly Trp Thr Arg Glu Gly Asp Ser
435 440 445

Ser Ala Ala Lys Ser Gly Leu Ala Ala Leu Ile Thr Asp Gly Pro Gly
450 455 460

Gly Ser Lys Arg Met Tyr Ala Gly Leu Lys Asn Ala Gly Glu Thr Trp
465 470 475 480

Tyr Asp Ile Thr Gly Asn Arg Ser Asp Thr Val Lys Ile Gly Ser Asp
485 490 495

Gly Trp Gly Glu Phe His Val Asn Asp Gly Ser Val Ser Ile Tyr Val
500 505 510

Gln Lys